GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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W97764 standard; W97764 W97767 W9	1126 1126 1120 1120 1069 1069 1069 1045 989 984
W97764 standard; Protein; 396 N W97764; Py99 (first entry) 21-NAY-1999 (first entry) Sesert hedgehog; Dhh protein; hy ptc therapeutic; patched; signal Huntington's disease; amyotroph: cerebral ischaemia; hypoxia; ne Homo sapiens. W9990475-A2. 04-FEB-1999: U5419. 24-UUL-1998; U5419. 24-UUL-1997; US-900220. (ONTO-) ONTOGENY INC. Mahanthappa NK, Miao N, Pang K, WPI, 99-142578/12. N-PSDB; X07270. Increasing the survival of neuron cells - by using a ptc therapeut inhibitor, or an agent derived in the treatment of parkinson's dis- cells - by using a ptc therapeut inhibitor, or an agent derived in the treatment of parkinson's dis- cells - by using a ptc therapeut inhibitor, or an agent derived in the treatment of parkinson's dis- cells - by using a ptc therapeutical in the treatment of parkinson's dis- invention is based on the finding in the treatment of parkinson's disease (both clair and/or GABA-nergic neurons, or is substantia nigra. Exemplary dis- tuntington's disease (both clair and cerebral ischaemia. The innoversequences) and ptc therapeutics of naturally occurring hedgehog poli- e.g. constructs oncoding recombi- trans-activation constructs for sequences) and ptc therapeutics of naturally occurring hedgehog that are effective in both human polypeptide comprising amino ac- The products can also be used for neurons in cultures, and to enhi- neurons in cultures, and to enhi- neurons in cultures, and to enhi- neuroprotective agent.	533.9 511.25.3.9 511.25.53.9 511.25.65.16.65.65.65.66.66.66.66.66.66.66.66.66.66
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       A new method to regulate muscle growth

3) isclosure; Page 121-121; 130pp; English.

2) The present sequence is human Desert hedgehog protein Dhh. The Invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in least the engage of the repetit (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy atrophy or cardiac on colaimed). The hedgehog therapeutic can hyperblastic or neoplastic growth of muscle tissue such as in myopathy comprises at least a bloactive extracellular portion of a hedgehog protein (see v05510-19) encoded by a vertebrate hedgehog gene (see x25098-107), especially a human hedgehog gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                  74-MAR-1999; U17922.
29-AUG-1998; U5-057394.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
31adgen CS, CUITIE PD, Hughes SI
WPI; 99-243557/20.
N-PSDB; X25105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Desert hedgehog protein; human; hedgehog therapeutic; Desert hedgehog; Dhh protein; human; hedgehog therapeutic; patched; signal transduction; muscle atrophy; cachexia; muscular myopathy; myoblastic sarcoma; therapy.
Sequence
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MALLTNLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS 60

Query Match
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Score 2088; DB 1; Pred. No. 1.1e-216; ; Mismatches 0;

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Gaps

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Query Match
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Matches 394; Conservative

99.8%;

Score 2083; DB 1; Pred. No. 3.7e-216; 1; Mismatches 1;

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This is the amino acid sequence of a precursor of a novel human Desert hedgehog protein, as deduced from a CDNA clone (see V62395) derived from cell line ARH-77 (ATCC CRL-1621). The mature form (see W79593) of the hedgehog protein is also claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein. The hedgehog protein is useful in establishment of hybriddomas which produce antibodies recognising the protein, and the MAb is useful for detecting and purifying the protein. The hedgehog protein burseful in establishment of hybriddomas which produce antibodies recognising the protein. The hedgehog protein burseful in establishment of hybriddomas which produce and mab can be used to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses. Sequence 396 AA;
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N-PSDB; V62395.
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25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU
Ariyasu T, Nakamura S, Orita
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                                                                                            Query Match
Best Local S
Matches 382
                                                                                                                                                                                                                                                           Claim 17: Page 135-37: 210pp; English.

The sequence represents a mouse Indian hedgehog protein, homologout to a Drosophila hedgehog protein (R77337), and is encoded by a cDN isolated by low stringency screening of a mouse genome DNA library Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic c
                                                                                                                                                                                                                                                                                                                                                                                                                                therapy.
Claim 17; Page 135-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ingham PW, Mcmahon WPI; 95-255060/33. N-PSDB; Q91642.
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Mouse desert hedgehog protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hedgehog-like protein(s)
to treat degenerative ner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; desert hedgehog
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hes 382;
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-1993; US-176427.
-1994; US-356060.
) HARVARD COLLEGE.
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPERIAL CANCER
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396 AA
                                                                                            96.2%;
nilarity 96.5%;
Conservative
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Tabin CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rotein; probe; primer;
gene therapy; antibody
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rvous system disorder(s) and in gene
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                                                                                            score 2008; DB 1;
Pred. No. 4.5e-208;
5; Mismatches 8;
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                                Pri Method for limiting damage to neurons caused by ischaemic or epoxic pri conditions - is used for the treatment and prevention of e.g. conditions - is used for the transient ischaemic or epoxic pri cerebral infarction, stroke and transient ischaemic attacks Disclosure; Page 65-66; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by cischaemic or epoxic conditions by administering a ptc (patched); cc construct which recombines with the genomic hedgehog gene to provide a cc neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a cc erebral tissues against ischaemic linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect correbral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic corresponding introducing the demacy other cases of conditions may cause cerebral hypoxia, or progressive loss of neurons conditions may cause cerebral hypoxia, or progressive loss of neurons conditions may cause cerebral hypoxia, or progressive loss of neurons cured treatment reduces CIV by at least 25, particularly at least 70,%. The converse of the present sequence represents a hedgehog sequence given in the present correspondence correspondence and engage of the progressive and the present correspondence represents a hedgehog sequence given in the present correspondence correspondence and correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgehog sequence given in the present correspondence represents a hedgeh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Dhh hedgehog protein sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

brain infarction; cerebral infarction; transient ischaemic attack;

stroke; cerebral infarct volume; spinal cord; oedema; trauma;

stroke; cerebral infarct volume; spinal cord; oedema; trauma;

haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahanthappa NK;
WPI; 99-095458/08.
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27-JUN-1997; US-883656.
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Query Match
Best Local Similarity
Matches 382; Conserv

Conservative

96.2%;

Score 2008; DB 1; Pred. No. 4.5e~208; 6; Mismatches 8;

Length

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Gaps

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PT increasing the survival of neuronal, dopaminergic and GABA-nergic PT cells - by using a ptc therapeutic such as a protein kinase pt inhibitor, or an agent derived from hedgehog polypeptides, useful in PT inhibitor, or an agent derived from hedgehog polypeptides, useful in PT the treatment of Parkinson's disease

PS Disclosure; Page 85-86; 138p; English.

CC This polypeptide is mouse Desert hedgehog protein (Dhh). The comparison of the finding that hedgehog proteins are useful compared to neurons or the general loss of dopaminergic neurodegenerative disorders resulting from the loss of dopaminergic cand/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, and creat in schaemia. The invention relates to hedgehog constructs (i.e. hedgehog polypeptides and gene therapy constructs agenerated is schemia. The invention relates to hedgehog resultatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) conflatures, and to enhance the implantation of such neuronal cells in conditions arising from the use of certain drugs, and in the conditions arising from the use of certain drugs, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mahanthappa NK, Miao N, Pang WPI; 99-142578/12. N-PSDB; X07272.
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24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
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W09904775-A2.
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A new method to regulate muscle growth

The Disclosure; Page 112-113; 130pp; English.

The present sequence is mouse Desert hedgehog protein Dhh. The

Convention relates to a method for modulating the formation and/or

cells, especially muscle stem/progenitor cells, in vitro or in

vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and

cene therapy constructs) or ptc therapeutic (i.e. a small organic

molecule that mimics the effect of hedgehog proteins on patched

signalling, or activates or potentiates patched signalling) in an

amount effective to alter the growth state of the treated cells.

Also claimed is a method for treatment or prevention of disorders

of, or surgical or cosmetic repair of, such muscle tissues, by

administering a hedgehog polypeptide or ptc therapeutic. The

disorder may be muscle atrophy, in particular skeletal muscle

catrophy or cardiac muscle atrophy, cachexia, or muscular myopathy

call claimed). The hedgehog polypeptide or ptc therapeutic can
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Best Local S
Matches 382
                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Desert hedgehog protein Dhh.

Mouse Desert hedgehog; Dhh protein; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atro
ptc therapeutic; patched; signal transduction; therapy.
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Sequence 396 AA;
                                                                                                                                                                                                                                                                            04-MAR-1999; U17922.
28-AUG-1999; US-057394.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, Ingham WPI; 99-243557/20.
N-PSDB; X25099.
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WO9910004-A2.
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Y05511;
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es 382; Conser
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Pred. No. 4.5e-208;
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                                                                                                                                                                                                                                                                                                                                                                         24-APR-1998;
14-APR-1998;
25-APR-1997;
                                                                                                                                                                                                  antibody Claim 3;
This is the amino acid sequence of a precursor of a novel human Desert hedgehog proteen, as deduced from a CDNA clone (see V62394) derived from cell line ARH-77 (ATCC CRL-1621). The mature form (see W7959) of the hedgehog protein is also claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detectin, a process for producing the protein, and a method for detecting the protein. The hedgehog protein is useful in establishment of hybridomas which produce antibodies recognising the protein, and the MAb is useful
                                                                                                                                                                                                                                                Human Desert hedgehog
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Ariyasu T, Nakamura S, Orita
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                                                                                                                                                                                                                          13-JUL-1995
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
14-DEC-1994; US-356060.
(HARD) HARVARD COLLEGE.
(IMCR) IMPERIAL CANCER R
Claim 17; Page 139-41; 210pp; English.
The sequence represents a mouse sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from an 8.5-day post coltum mouse library. Probes and primers derived from the sonic hedgehog
                                                                                                                                                                                   Ingham PW, Mcmaho
WPI; 95-255060/33
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       Method for limiting damage to neurons caused by ischaemic or epoxic conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks Disclosure; Page 68-70; 104pp; English.

A method has been developed for limiting the damage to neuronal cells ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.
                                                                                                                                                                                                                                                                                                  Mouse Shh hedgehog protein sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord; oedema; trauma; stroke; cerebral infarct volume; spinal cord; oedema; trauma;
                                                                                                                                                                                                                                                                                                                                                                  W94471;
29-APR-1999 (first entry)
                                                                                                                                                     N-PSDB; X16185
                                                                                                                                                                    Mahanthappa NK;
WPI; 99-095458/08.
                                                                                                                                                                                                                 26-JUN-1998; U13387.
27-JUN-1997; US-883656.
                                                                                                                                                                                                                                               07-JAN-1999
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                                                                                                                                                                                                                                                                                          haemorrhage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The present sequence represents a hedgehog sequence given in the present reventer.
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                            EELL 395
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                                                         AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAAQSATEARGAEPTAGIHWYSQLLYHIG
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Pred. No. 9.6e-123
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04-FEB-1999.
04-FEB-1999; U15419.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, 199142578/12.
N-PSDB; X07274.
                                                                                                                                                       21-MAY 1999 (first entry) protein. Mouse Sonic hedgehog (Shh) protein; mouse; dopaminergic; GAI Sonic hedgehog; Shh protein; mouse; dopaminergic; GAI ptc therapeutic; patched; signal transduction; Parkir Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia; hypoxia; neuroprotective; therap)
                                                                                                                                                                                                                                                  W97768;
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W09904775-A2.
Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase
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This polypeptide is mouse Shh Sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful, as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantial form.
05-JUL-1999 (first entry)
Mouse Sonic hedgehog protein Shh.
Sonic hedgehog; Sih protein; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
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Local Similarity
les 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHVSVKADNSLAVRAGGCFFGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLPLCCLALLA-----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG 61
                                                                                                                                                                                                                                                                         EELL 395
                                                                                                                                                                                                                                                                                                                                                                                                RLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                 AHRAFAPFRIAHALLAALAPARTDGGGGGSIPAAQSATEARGAEPTAGIHWYSQLLYHIG
                                                                                                                                                                                                                                                                                                                                                         AHRAFAPLRLLHA-LGALLP-----GGAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLDRDLQRRASEVAVETEWPPRKLLLIPWHLVFAA-----RGPAPAPGDFAPVFARRLRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
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llarity 58.7%;
Conservative !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exemplary disorders include Parkinson's disease, ase (both claimed), amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1217; DB 1;
Pred. No. 9.6e-123;
3; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                         -QPT-GMHWYSRLLYRLA
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Best Local
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W09910004-A2.

04-MAR-1999.

28-AUG-1998; U

29-AUG-1997; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-derived tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bloactive extracellular portion of a hedgehog protein (see Y05510-19) encoded by a vertebrate hedgehog gene (see X35098-107), especially a human hedgehog gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new method to regulate muscle growth Disclosure; Page 115-116; 130pp; English.
The present sequence is mouse Sonic hedgehog protein Shh. Th invention relates to a method for modulating the formation an maintenance of muscle tissue by ecotopically contacting muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD,
WPI; 99-243557/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells.
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419 TWLL
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                                   EELL
                                                                                                                                              QRVYVVAERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSW
                                                                                                                                                                                                                                                                                                                    RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
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                                                                                                                                                                                                                                                         FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAG
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                                                                        AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAAQSATEARGAEPTAGIHWYSQLLYHIG
                                                                                                                                                                                 DSVLA----PGGD-ALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQW
                                                                                                         AHRAFAPLRLLHA-LGALLP-----
                                                                                                                                                                                                                      FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP--
                                                                                                                                                                                                                                                                                              IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
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                                   395
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; US-057394.
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Pred. No. 9.6e-123;
3; Mismatches 82;
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                                                                                                           GGAV----
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                                                                                                           -QPT-GMHWYSRLLYRLA 391
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Scalaim 13; Pages 153-154; 210p; English.

CC This represents a mouse sonic hedgehog (shh) protein sequence. The CC Invention provides methods and compounds for modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary gland genes. The method for affecting cholesterol biosynthesis or transport in a cell comprises contacting a CC cell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing CC activity of a hedgehog polypeptide in cells, and for inducing pituitary gland gene expression utilises sequences selected from a zebrafish CC (shh) protein (W61486), a chicken shh protein (W61487) or a mouse shh cc (shh) protein (W61488). The products and methods provide for compounds which CC can affect hedgehog activity. They can be used for treating disorders which arise from neuronal degeneration or abnormal function. They can class be used for treating during the healing of major limb trauma. They can sloo be used for treating during the healing of major limb trauma. They can compound the content of the products can also be used for detection and diagnosis.
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Best Local Similarity
Matches 248; Conserv
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WO9830576-A1.

16-JUL-1998.

07-OCT-1997; U15753.

02-OCT-1997; US-061323.

07-OCT-1996; US-729743.

(UYJO) UNIV JOHNS HOPKINS SI
BEACHY PA. POTTET JA;

WPI; 98-399053/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hedgehog-derived poly:peptide(s) - used to develop products modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse sonic hedgehog (shh) protein.
Hedgehog polypeptide; neuronal cell proliferation; zebrafish; shh;
cholesterol blosynthesis; pituitary gland gene expression; mouse;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
neuronal degeneration; nerve-sparing agent; Smith-Lemli-Optiz syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W61488 standard; Protein; 437
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                                                                                                                                      FLDRDLQRRASEVAVETEWPPRKLLLITPWHLVFAA----RGPAPAPGDFAPVFARRLRAG 297
                                                                                                                                                                                                                  RLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLPLCCLALLA-----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG 61
AHRAFAPLRLLHA-LGALLP--
                                       QRVYVVAERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSW
                                                                                                                                                                                                IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
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                                                                                                                                                                                                                                                                                                                                                             RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                          DSVLA---PGGD-ALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQW 352
                                                                                                               FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                       LLARCFLVILASSLLVCPGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASG 61
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Pred. No. 2e-122;
4; Mismatches 8
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-GGAV--
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-QPT-GMHWYSRLLYRLA 391
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                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                 Claim 17; Page 133-35; 210pp; English.
Claim 17; Page 133-35; 210pp; English.
The sequence represents a chicken sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from a stage 22/22 limb bud cDNA library. Probes and priners derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used 1 gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.

Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-UUI-1995
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
30-DEC-1994; US-356060.
14-DEC-1994; US-356060.
(IMRD ) HARVARD COLLEER RES TECHNOLOGY
(IMR) TWEERIAL CANCER RES TECHNOLOGY
(ING) TWEERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken sonic hedgehog protein.

Chicken; sonic hedgehog protein; stage 22/22 limb bud; probe; primer; diagnostic; nervous system disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hedgehog-like protein(s) and nucleic to treat degenerative nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-255060/33.
N-PSDB; Q91636.
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R77338;
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                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                    DFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN
                                                                 SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT
                                                                                                                                                                                                                                    MALLTNLLP----LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL
                                                SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
                                                                                                                                                                                                             MLLLTRILLVGFIC - - ALLVSSGLTCGPGRG - IGKRRHPKK - LTPLAYKQFIPNVAEKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLLFLDRDLQRRASEVAVETEWPPRKLLLTPWHLVFAA--RGPAPAPGDFA--PVFARR
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                                                                                                                                                                                                                                                              57.4%;
ilarity 59.4%;
Conservative 5
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27. .3;
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                                                                                                                                                                                                                                                            Score 1198; DB 1;
Pred. No. 1e-120;
Vicamatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence (R77349)"
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disorder(s) and in gene
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DR WPI; 99-995458/08.

DR WPIS; 99-995458/08.

DR W-SDB; X16182.

PT Method for limiting damage to neurons caused by ischaemic or epoxic PT conditions - is used for the treatment and prevention of e.g. PT cerebral infarction, stroke and transient ischaemic attacks pt cerebral infarction, stroke and transient ischaemic attacks pt cerebral infarction, stroke and transient or neuronal cells by cischaemic or epoxic conditions by administering a ptc (patched) construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which resolution regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic construct with the brain or spinal cord, codema caused by trauma, haemorrhage and tenephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The corporation.

CC invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.4
Best Local Similarity 59.4
Matches 244; Conservative
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07-JMN-1999; U13387.
26-JUN-1997; US-883656.
27-JUN-1997; US-883656.
(ONTO-) ONTOGENY INC.
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Chicken Shh hedgehog protein sequence.
Chicken Shh hedgehog; ptc therapeutic; neuroprotective; neuronal cell;
Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;
brain infarction; cerebral infarction; transient ischaemic attack;
stroke; cerebral infarct volume; spinal cord; oedema; trauma;
haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
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SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
                                                                                                                                           SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT 237
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В
                                                                  351 QWAHRAFAPIRILHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL 395
360 SWAHWAFAPERLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
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Search completed: June Job time: 2585 sec 'n 2000, 08:16:20

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Result
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Maximum DB seq
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Gapop 10.0 , Gapext 0
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Copyright (c) 1993 - 2000 Comp
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sp_unclassified:*
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096699
1 Q9WUP6
3 042128
3 Q9YGU3
3 Q9YGU3
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Q9W6C1
  042234
P91573
Q9XV14
Q9XUV2
Q22872
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Q9xs16 bos taurus
Q9xs16 bos taurus
Q9w6C1 eleutheroda
Q9y97 ambystoma m
Q96699 junonia coe
Q9wup6 rattus norv
Q42128 oryzias lat
Q9y9u3 brachydanio
Q42441 oryzias lat
Q42234 coturnix co
P91573 caenorhabdi
Q9xv14 caenorhabdi
Q9xv2 caenorhabdi
Q9xv2 caenorhabdi
Q9xv2 caenorhabdi
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057404 pleurodeles
Q9w7q9 paralichthy
073803 fugu rubrip
017499 branchiosto
061676 lytechinus
                                                                                                                                                                                                                                                        Description
                                                                                                                                                        Q9wv29 rattus norv
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RESULT
O57567
ID O5766
AC O56
AC O56
AC O57

Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus

FERRETTI P.;

SEQUENCE FROM N.A.

STARK D.R., GATES P.B., BROCKES J.P., FE
Dev. Dyn. 0:0-0(1998).

EMBL; AF047466; AACO3108.1; -.

HSSP; Q62226; IVHH.

BFAM; PF01079; H1nt; 1.

PFAM; PF01079; H1nt; 1.

PRINTS; PR00632; SONICHHOG.

SEQUENCE 406 AA; 45072 MW; 9DOFFA76

9D0FFA76 CRC32;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
94.5	95	95	95	95.5	95.5	96	96.5	96.5	97	97	86	98.5	99	100.5	102	105	123.5	138.5	138.5	140	148	148.5	154.5	161
4.3	4.4	4.4	4.4		4.4				4. 5			4.5	4.6		4.7	٠			6.4				7.1	
257	2117	1616	950	846	299	8563	647	54	7463	1551	1222	316	1013	478	751	1997	205	629	550	557	485	481	1207	1226
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Q9Y2U4	Q9Z4Z9	P96285	Q50470	053152	Q9Y6K2	Q54297	039278	042233	Q9Z4X6	Q14160	Q9YC75	Q9ZBV4	053499	043955	Q21754	005647	Q23193	045273	Q94130	Q94129	Q94128	045992	Q21535	Q21835
		P96285 mycobacteri		O53152 mycobacteri		Ç2		w		Q14160 homo sapien			O53499 mycobacteri	043955 leishmania	Q21754 caenorhabdi			045273 caenorhabdi			Q94128 caenorhabdi	045992 caenorhabdi	Q21535 caenorhabdi	Q21835 caenorhabdi

ALIGNMENTS

O57567 PRELIMINARY; PRT; 406 AA. 057567; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) HEDGEHOG SEGMENT POLARITY HOMOLOG.

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AKTG	AKTG	HHSD	HHSE	FKEL	FKEI	LLL	LIL	292	atch
GCFP	4409)	ESLH	ESLH	TPNY	TPNY	GPGA	VPAA	0,1	3
ARAL!	AGAQ\	YEGRA	YEGRA	NPDI	NPDI	Lecei	WGCGI	onsei	Query Match
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GEKI	GARV!	TSDRI	TSDRI	ENTG	ENTG!	GRRPI	GSRRI	ve *	0.88
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EPGHE	RPGDI	GMLAI	GLLAI	TORCE	TORCE	LIPLS	LVPL!	Misn	ore 1
VLCM	VLΑM	LAAE	LAVE	ORLN	ORLN	YKOF	YKOF	Matches 292; Conservative 31; Mismatches 69;	70.8%; Score 1539; DB 13;
DEGGI	GEDGS	AGEDV	AGFD	SLAIS	SLAIS	LPHVI	SPNVI	Se .	2 B
RTYS	PTFS	VYYE	WYYE	ONWA	ONWA	EKHL	EKIL	69,	13;
194 AKTGGCFPARALATLESGEKIPIADLEPGHRVLCMDEGGRRTYSDFLTFLDRDSTAVKEF 253	198 AKTGGCEPAGAQVRLESGARVALSAVRPGDRVLANGEDGSPTFSDVLIFLDREPHRLRAF 257	134 HHSDESLHYEGRAVDITTSDRDRNKYGMLARLAAEAGFDWVYYESKAHIHCSVKSEHSAA 193	138 HHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAA 197	74 FKELTPNYNPDIIFKDEENTGADRIMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDG 133	78 FKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDG 137	15 LLLGGPGALGCGPGRVIGRRPRPPR-LIPLSYKQFLPHVPEKTLGASGRYEGKIARNSER 73	18 LLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIARSSER 77	Indels	Leng
LDRD	LDRE	HCSVI	HCSV	LRVT	LRVT	YEGK	YEGK	ls	Length 406;
STAVK	PHRLR	KSEHS	KSEHS	EGWDE	EGWDE	IARNS	IARSS	2;	06;
EF 2!	AF 2	AA 1:	AA 1) G 1	- DG 1	ER 7	ER 7	2; Gaps	
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RESULT
ID 77404
AC 00
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RESULT
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ID Q9
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Best Local S
Matches 255
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTAL NICOLAS S., LE PARCO Y.
SUBMITTAL NICOLAS S., LE PARCO Y.
SUBMITTAL NICOLAS S., LE PARDLY C.
EMBL; AF003532; AAB94412.1; -.
HSSP; 062226; 1VHH.
HSSP; 062226; 1VHH.
R PEAM; PF01085; HH_S1gnal; 1.
R PEAM; PF01079; Hint; 1.
R PEAM; PF01079; Hint; 1.
R PEAM; PF01079; Hint; 1.
R PEAM; PF01079; HOT; 1.
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O57404;
O57404;
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O57404;
O1-701-1998 (TrEMBLrel. 05, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SONIC HEDGEHOG-RELATED PROTEIN.
  Q9W7Q9
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Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Pleurodeles.
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                                                                                                                         GFGILSFFSPQDYSSHSPPAPSQAEGVHWYSEILYRIGTWVLQADTIHPLGMAAKSS
                                                                                                                                                                                                                       REGRGLREATVDRVYLEEATGAYAPVTAHGTVVIDRVLASCYAVIEEHSWAHWAFAPLRV
                                                                                                                                                                                                                                              VP--GLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCEAAVADHHLAQLAFWPLRL 366
                                                                                                                                                                                                                                                                                                                     IETSLPRERLRLTAAHLLFVAQEHPGNASAGNFRSKFGHRRFRSMFASSVRPGHRVLTED
                                                                                                                                                                                                                                                                                                                                            IETQDPPRRLALTPAHLLFTADNHTEPAA------RFRATFASHVQPGQYYLVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 59.1%;
Similarity 61.2%;
55; Conservative
                                                                                                                                                   -FHSLAWGSWTP-----GEGVHWYPQLLYRLGRLLLLEEGSFHPLGMSGAGS
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
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Pred. No. 1.1e<sup>o</sup>
46; Mismatches
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  PRT;
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  414
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1.1e-96;
hes 90;
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Best Local S
Matches 251
                                                                                                                                                                                                                                                O73803 PRELIMINARY;
O73803;
O1-AUG-1998 (TrEMBLrel. 0)
O1-AUG-1998 (TrEMBLrel. 0)
O1-NOV-1999 (TrEMBLrel. 1)
FUGU HEDGEHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 99
SUZUKI T.,
                       SEQUENCE FROM N.A.
GELLNER K., BRENNER S.;
Submitted (MAR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHH.
Paralichthys olivaceus (Flounder).
Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Neopterygii; Teleostei; Euteleostei; Bothidae; Paralichthys.
                                                                                                                                                                                                                                 FHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxd-4 expression in the pharyngeal area and induces skeletal malformation in flounder (Paralichthys olivaceus) embryos."; Dev. Growth Differ. 41:143-152(1999).
EMBL; AB029748; BAA82360.1; -.
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                           Fugu rubripes (Japanese pufferfish) (Takifugu rubripes),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Relosatei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWGSWTPG----EGVHWYPQLLYRLGRLLLEEGSFHPLGMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFSSQPQASAQKDGVHWYSKILYQLGTWLLDSHSIHPLGMS
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     AF056116;
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Similarity 62.6%;
51; Conservative '
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99238226.
C., ICHIRO O.,
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     AAC34384.1;
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, Last annotation
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Last annotation update)
                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 5.6e-95;
17; Mismatches 92;
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                              Query Match
Best Local S
Matches 215
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Best Local :
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                                                                              SHIMELD S.M.;
SUBDITTED (JUN-1997) to the EMB
EMBL; Y13858; CAA74169.1; -
HSSP; Q62226; IVHH.
PFAM; PF01079; HILT; 1.
PFAM; PF01079; HILT; 1.
PRINTS; PR00632; SONICHHOG.
SEQUENCE 415 AA; 46765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q62226; 1VHH.
PFAM; PF01085; HH_si
PFAM; PF01079; Hint;
SEQUENCE 442 AA;
                                                                                                                                                                                  Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                  AMPHIHH
                                                                                                                                                                                                                             AMPHIHH PROTEIN.
                             Local Sim thes 215;
                                                                                                                                                                                                                                                                                                                                433 IVLNPDLFHP 442
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                                                                                                                                                                                                                                                                                                                                           LLLEEGSFHP 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFNELVCNYNPDIVFKDEENTNADRFMTKRCKDCLNRLALAVMNQWPGVHLRVTEAWDED
                              Similarity 53.3
15; Conservative
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                                                                                                                                                                                                                                                                               PRELIMINARY;
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; Hint; 1.
2 AA; 49286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49286 MW;
                                        49.5%;
                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                             ; Score 1076.5; DB
; Pred. No. 9.1e-80;
46; Mismatches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1086.5;
Pred. No. 1.5
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                                                                                C5BAC408 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                             415
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L.5e-80;
hes 98; I
                               127;
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                              Indels
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                              15;
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RESULT
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Best Local Similarity 48.2
                                                                                                                                                                                                                                                                                                                                 HERTZLER P.L., MCCLAY D.R.;
Submitted (APR-1998) to the EMB:
EMBL; AFG59606; AAC15065.1; -.
HSSP; Q62226; IVHH.
PFAM; PF01079; Hint; 1.
PFAM; PF01079; Hint; 1.
PRINTS; PR00632; SONICHHOG.
SEQUENCE 410 AA; 46071 MW;
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061676;
01-AUG-1998
01-AUG-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytechinus :
Eukaryota;
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPGLQPARVAAVSTHVALGAYAPLIKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEGWDEDGHHSEESLHYEGGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCS
                                                                                                                                                                        RSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEG
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DSTLFYVIETED-KTIVQLTPQHLIYVSERESN-FDQSRAVFASEVRTNQFVYTTAQNHD
                                                   ESAAAKNSGGCFPGFSQAYLKNGRMISMLDIRVGDEVAVVNNNGELDYSDVIMIVHRKLN
                                                                  EHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPH
                                                                                                                                                           RDDERFSKLSPNNNDDIVFKDEEGTGADRLMTQRCKDKLNTLAISVMNEWPGIKLRVVEA
                                                                                                                                                                                                               CLIAL----TQACHPGR-SGKTSHRPRNRTPLQYKQKVPNISEDTFGASGPPEGRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLV--A 307
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                         RLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                  42.0%; Score 914; DB 5;
48.2%; Pred. No. 1.5e-66;
tive 62; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                     48F9B973 CRC32;
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                                                                                                                                                                                                                                                                    124; Indels
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                Q9XS16
Q9XS16;
Q9XS16;
Q1-NOV-1999 (TIEMBLIFEL 12, C:
Q1-NOV-1999 (TIEMBLIFEL 12, LI
Q1-NOV-1999 (TIEMBLIFEL 12, LI
Q1-NOV-1999 (TIEMBLIFEL 12, LI
SONIC HEDGEHOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9WV29 PRELIMINARY: PRT;
O9WV29;
O1-NOV-1999 (TrEMBLrel 12, Created)
O1-NOV-1999 (TrEMBLrel 12, Last sec
O1-NOV-1999 (TrEMBLrel 12, Last and
INDIAN HEDGEHOG PROTEIN (FRAGMENT).
                                         KOYAMA E., IWAMOTO M., OHMORI T., KURISU K., WU C., OO BASHIR M.M., TUCKER T., PACIFICI M.;
"Development of Stractum Intermedium and its Role as a Signaling Structure During Odontogenesis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ database EMBL; AF144100; AAD33926.1;
                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Run
NON_TER
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Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Muridz
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Submitted (JUN-1999) to the EEMBL; AF162914; AAD45372.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY; GARGES P.L., MEYER R.A. JR., BROWN C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                         TISSUE-TOOTH GERM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRN 161
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96.6%;
                                                                                                                                                                                                                                                                                 ta; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
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Last annotation update)
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ae; Murinae;
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.9e-66;
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                                                                                                                Sonic Hedgehog-
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Best Local S
Matches 125
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Best Local
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                                   Q9YGV7

Q9YGV7;
Q9YGV7;
01-MAY-1999 (TrEMBLrel. 10, 0
01-MAY-1999 (TrEMBLrel. 10, 1
01-NOV-1999 (TrEMBLrel. 12, 1
SONIC HEDGEHOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W6C1
Q9W6C1;
01-NOV-1999
01-NOV-1999
01-NOV-1999
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eleutherodactylus coqui.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
                    Ambystoma mexicanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TIEMBLIEL 12, Created)
01-NOV-1999 (TIEMBLIEL 12, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
50NIC HEDGEHOG PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differences in vertebrate limb
                                                                                                                                                                                                                                                                                174 GFDWVYYESKAHVHCSV 190
                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Sines 125;
                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 N
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                                                                                                                                                                                                                                                                                                                                          GFDWVYYESKAHIHCSV 138
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||:||:||:||:||:||:||:||:||
KDKLNALAISVMDQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYKQFSPNVPEKTLGASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLAVEAGFDWVYYESKAHI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLAVEAGFDWVYYESKAHV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t developing frog E. coqui.";
tted (DEC-1998) to the EMBL/GenBank/DDBJ databases
AF113403; AAD23436.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRC
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138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICHARDSON M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
15751 MW;
                      (Axolotl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15961 MW;
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 681; DB 13;
Pred. No. 2.8e-48;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 701; DB 6;
Pred. No. 6.7e-50;
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Craniata;

Vertebrata; Amphibia;

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RESULT

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DT 011

DT 011
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOROK M.A., IZPIZUA-BELMONTE J.C., GARDINER D. Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF031480; AAD18128.1; -. HSSP; Q62226; 1VHH. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Junonia coenia (Peacock butterfly) (Precis coenia).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEDGEHOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Batrachia; Caudata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evolution.";
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POHNSON R.L., GATES J., SCC
Recruitment of a hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSVKSEHSAAAKTGGCFPAG
  123
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; AF117742; AADON
; Q62226; 1VHH.
TER 1
                                                                                  AQVRLESGARVALSAVRPGDRVLAMGEDG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAVDITTSDRDRSKYGMLARLAVEAGFDWVYFESKAHIHCSVKAENSVAAKSGGCFPAS
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                                                                                                                                                                                              ASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKVTLEHGVTRPVKDLRPGDRVLAADGQG 149
  RSYIHCSVKTESSVG--TGAGCFPSGAVVHTENGP-XDIASLKKGNKVLA
                                                                                                                                                                          ASGPPEGRITRDDEKFRDLVPNYNPDIDFKDDEGTGADRLMTQRCKEKLNTLAISVMNQW
                                         KAHVHCSVKSEHSAAAKTG-GCFPAGAQVRLESGARVALSAVRPGDRVLA 231
                                                                                                                                                                                                                                                                                   Similarity
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150 AA;
                                                                                                                                                                                                                                                                                                                                                                         185
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD08931.1;
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16599
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                                                                                                                                                                                                                                                                             27.4%;
                                                                                                                                                                                                                                                                                                                                                                           20745 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SELEGUE J.E., PEARSON B.J., SCOTT M.P., CARROLL S.B.; ehog regulatory circuit in b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                               Score 597; DB Pred. No. 2.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 665; DB 13;
Pred. No. 6.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9356329B CRC32;
                                                                                                                                                                                                                                                                                                                                                                           96A09B5A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                 DB 5,
2.9e-41;
25;
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                                                                                                                                                                                                                                                                                                      Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                butterfly eyespot
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RESULT
042128
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Best Local S
Matches 91
                               Query Match
Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Desert hedgehog in the rat.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ (EMBL; AF148226; AAD31927.1; -NON_TER 129 129 SEQUENCE 129 AA; 14879 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9WUP6;
Q9WUP6;
01-NOV-1999
01-NOV-1999
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042128;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Fiitheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHH.
                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                           Submitted (SEP-1997) to the EMBL; AB007129; BAA22368.1; HSSP; Q62226; IVHH.
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha; Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                        STRAIN-BBRR;
                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                Oryzias latipes (Medaka fish).
                                                                                                                                                                                                                                            ME-SHH.
                                                                                                                                                                                                                                                     SHH, PARTIAL
                                                                                                                                                ARAKI K.;
              128
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RVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVH 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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                              Similarity 70.6
84; Conservative
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119 t
                                                                                                                                                                                                                                                     (TYEMBLrel. 05, Created)
(TYEMBLrel. 05, Last sequence update)
(TYEMBLrel. 12, Last annotation updat
L CDS (FRAGMENT).
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(TrEMBLrel. 12, Last se
(TrEMBLrel. 12, Last an
EHOG PROTEIN (FRAGMENT).
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TISSUE-WHOLE EMBRYO;
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13179 þ
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                                          21.7%;
70.6%;
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                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510.5; DB 11;
Pred. No. 1.9e-34;
0; Mismatches 13;
                               Score 472; DB 13;
Pred. No. 2.3e-31;
7; Mismatches 18;
                                                                                  1CAE5021 CRC32;
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                               Indels
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Rattus.
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RESULT
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ID 22
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                        042441 PRELIMINARY; PRT; 80 AA.
042441;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
50NIC HEDGEHOG (FRAGMENT),
07yzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryzinae;
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"Zebrafish hox clusters and vertebrate genome evolution.";
Science 282:1711-1714(1998).
EMBL; AF071236; AAD15931.1; -.
EMSP; Q62226; 1VHH.
                                                                                                                        EMBL; Z97019; CAB09695.1; -. HSSP; Q62226; IVHH. PFAM; PF01085; HH_signal; 1.
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AMORES A., FORCE A., YAN Y.-L., WANG Y.-L., FRITZ A., PRIN HO.R., AMEMITA C., LANGELAND J., WESTERFIELD M., EKKER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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01-NOV-1999
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

KOESTER R., STICK R., LOOSLI F., WITTBRODT J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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|||:||||||||:||| |||||:
LLAQLAVEAGFDWVHYESKYHVHCSVKA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSVKSEHSAAAKTGGCFFAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSVKAESSVAAKSGGCFPGSSTVTLENGTQRPVKDLQPGDRVLAADYDGNPVYTDFIMF 119
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9180 MW;
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    Created)
    Last sequence update)
    Last annotation updat

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Pred. No. 1.9e-25;
5; Mismatches 10;
            59BE42B8 CRC32;
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Matches
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                           61
                                                                 Local
ITTSDRDKSKYGTLSRLAVE
       ITTSDRDRNKYGLLARLAVE
                                                          17.9%;
l Similarity 90.0%;
72; Conservative
80
              172
                                                          Score 389; DB 13;
Pred. No. 7.3e-25;
5; Mismatches 3;
                                                                        Length 80;
                                                           Indels
                                                           0
                                                          Gaps
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Search completed: June 5, 2000, 08:19:30 Job time: 184 sec

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Result
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121 QWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYY 180

Query Match
Best Local Similarity 100.

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therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic of attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The present sequence represents a hedgehog sequence given in the present sequence. 411 AA;	equence. peutic; neuroprotective; repeutic; neuroprotective; ransient ischame; spinal cord; oedema; me; spinal cord; oedema; is; coronary bypass; cerelis; cerelis; coronary bypass; cerelis;	W61487 R77345 W94469 W957766 Y05511 W97764 W79595 W79595 W79597 W94477
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                       DR N-PSDB; x07259.

PT Increasing the survival of neuronal, dopaminergic and GABA-nergic reals - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in pt inhibitor, or an agent derived from hedgehog polypeptides, useful in pt the treatment of Parkinson's disease

CC laim 30; Page 95-97; 138pp; English.

CC laim 30; Page 95-97; 138pp; English.

CC laim 30; Page 95-97; 138pp; English.

CC as protective agents in the treatment and prophylaxis of neuronedgenerative disorders resulting from the loss of dopaminergic neurons; or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, and cerebral ischaemia. The invention relates to hedgehog constructs encoding recombinant hedgehog polypeptides and creament and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and conformable of the substantially occurring hedgehog proteins on patched signalling) constructs of naturally occurring hedgehog proteins on patched signalling) conformable comprising amino acids 28-202 of human 1hh is preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurons constructs argent of hypoxia, e.g. as a construct or constructs and in the prevention and/or treatment of hypoxia, e.g. as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, Pang K, Wang M;
WPI; 99-142578/12.
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W97763;
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commaintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in converse therapy constructs) or put cherapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or put cherapeutic (i.e. a small organic collecule that mimics the effect of hedgehog proteins on patched comblecule that mimics the effect of hedgehog proteins on patched common effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy calimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic can composite the common 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new method to regulate muscle growth
Disclosure; Page 120-121; 130pp; English.
The present sequence is human Indian hedgehog protein Ihh. The
invention relates to a method for modulating the formation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-24557/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Indian hedgehog protein Ihh.
Indian hedgehog; Ihh protein; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atro
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
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29-AUG-1997; US-057394.
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Indels Length

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Gaps

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411;

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Query Match Best Local Similarity

100.0%; llarity 100.0%; Conservative (

0

Score 2175; Pred. No. 1.1 0; Mismatches

Matches

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PT Method for Inimiting damage to neurons caused by ischaemic or epoxic PT conditions - is used for the treatment and prevention of e.g. conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks Disclosure; Page 66-68; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by CI ischaemic or epoxic conditions by administering a ptc (patched) cC ischaemic or epoxic conditions by administering a ptc (patched) cC neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a cerebral tissues against ischaemic linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic cases of conditions may cause cerebral hypoxia, or prophylactic in many other cases of conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The present is conditions a hedgehog sequence given in the present conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume, spinal cord; oedema; trauma; haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
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                                                                                                                                                                                                                                                                                                                                                            N-PSDB; X16184.
                                                                                                                                                                                                                                                                                                                                                                           Mahanthappa NK;
WPI; 99-095458/08.
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27-JUN-1997; US-883656
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PS Disclosure; Page 87-88; 138pp; English.

CC This polypeptide is mouse Ihh Indian hedgehog protein. The CC invention is based on the finding that hedgehog proteins are useful CC as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic CC and/or GABA-nergic neurons, or the general loss of tissue from the CC substantia nigra. Exemplary disorders include Parkinson's disease, CC Huntington's disease (both claimed), amyotrophic lateral sclerosis CC and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene treats activation constructs for altering hedgehog gone regulatory C sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling)
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24-JUL-1998;
24-JUL-1997;
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W97767;
21-MAY-1999
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Mahanthappa NK, Miao N, Pang
WPI; 99-142578/12.
                                                                                                                                                                                                                                                                                              N-PSDB; X07273.
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Mouse Indian hedgehog (Inh) protein.
Indian hedgehog; Ihh protein; mouse; dopaminergic; GABA-ner ptc therapeutic; patched; signal transduction; Parkinson's Huntington's disease; amyotrophic lateral sclerosis;
Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful the treatment of Parkinson's disease
                                                                                                                                                                                                                                                                                                                        cerebral ischaemia; hypoxia; neuroprotective;
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Pred. No. 5.3e-200;
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Best Local
Matches 38
                                                                                                                                                                       04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, I
WPI; 99-243557/20.
N-PSDB; X25100.
A new method to regulate muscle growth Disclosure; Page 114-115; 130pp; English.
The present sequence is mouse Indian hedgehog protein Ihh. The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells.
                                                                                                                                                                                                                                                                                                    05-JUL-1999 (first entry)
Mouse Indian hedgehog protein Ihh.
Indian hedgehog; Ihh protein; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
                                                                                                                                                                                                                                                               04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that are effective in both human and animal subjects. Human Ihh and by preptides (see W97763-64) are preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                           105512 standard; Protein;
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Similarity 94.6%;
89; Conservative :
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Pred. No.:5.3e-200;
10; Mismatches 12;
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FWPLRLFPSLAWGSWTPSEGVHSYPQMLYRLGRLLLEESTFHPLGMSGAGS
                                                    SDVLIFLDREPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQP
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RR7250LT RR7
therapy.

Claim 17; Page 137-38; 210pp; English.

The sequence represents a mouse Indian
to a Drosophila hedgehog protein (R773
                                                                                                                                                                      N-PSDB; Q91640.

Hedgehog-like protein(s) and nucleic acid(s) encoding to treat degenerative nervous system disorder(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1994; U14992.
30-DEC-1993; US-176427
14-DEC-1994; US-356060
                                                                                                                                                                                                                                                                                                                                                           (HARD ) HARVARD COLLEGE
(IMCR ) IMPERIAL CANCER
Ingham PW, Mcmahon AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus. WO9518856-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; Indian hedgehog protein; probe; nervous system disorder; gene therapy;
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95-255060/33.
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antibody.
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Indian hedgehog protein, (R77337), and is encoded

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Matches
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WPI; 95-255060/33.
W-PSDB; 091641.
                   Claim 17; Page 146-47; 210pp; English.

Claim 17; Page 146-47; 210pp; English.

The sequence represents a mouse Indian hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated by screening of a human fetal lung 5'-stretch plus cDNA library. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene antibodies generated from the protein may be used as
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                                                                                                                                                                 Hedgehog-like protein(s) and nucleic acid(s) encoding them to treat degenerative nervous system disorder(s) and in gene
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
W09518856-A1.
                                                                                                                                                                                                                                                                                                                                                                       Human; Indian hedgehog protein; probe; mervous system disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                       Human Indian hedgehog protein
Human; Indian hedgehog proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                     R77344 standard;
                therapeutic
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hes 319;
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US-356060.
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                research
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Pred. No. 6.6e-164;
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                                                                                                                                                                                                                                                                                                                                                                                       diagnostic;
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          pr gland gene(s)

Schlim 13: Pages 153-154; 210pp; English.

CC laim 13: Pages 153-154; 210pp; English.

CC laim 13: Pages 153-154; 210pp; English.

CC claim 13: Pages 153-154; 210pp; English.

CC differentian provides methods and compounds for modulating proliferation or compounds for modulating proliferation or compound that compounds for modulating proliferation or compression of pituitary gland genes. The method for affecting cholesterol biosynthesis or transport in a cell comprises contacting a ccell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing activity of a hedgehog polypeptide in cells, and for inducing pituitary claim gene expression utilises sequences selected from a zebrafish ctiggy-winkle hedgehog (twhh) protein (W61485), a zebrafish sonic hedgehog (shi) protein (W61486), a chicken shh protein (W61487) or a mouse shh compound the products and methods provide for compounds which can affect hedgehog activity. They can be used for treating disorders which arise from neuronal degeneration or abnormal function. They can also be used for treating smith-Lemil-Optiz syndrome. The products can so be used for treating smith-Lemil-Optiz syndrome. The products can so be used for detection and diagnosis.
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Best Local
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07-0CT-1997; U15753.
02-0CT-1997; US-061323.
07-0CT-1996; US-729743.
(UYJO ) UNIV JOHNS HOPKINS S
Beachy PA, Porter JA;
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20-OCT-1998 (first entry)
20-OCT-1998 (first entry)
Mouse sonic hedgehog (shh) protein.
Mouse sonic hedgehog (shh) protein.
Hedgehog polypeptide; neuronal cell proliferation; zebrafish; shh;
cholesterol blosynthesis; pituitary gland gene expression; mouse;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
tiggy-winkle hedgehog protein; smith-Lemli-Optiz syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 98-399053/24.

New hedgehog-derived poly:peptide(s) - used to develop products modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
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Best Local (
The sequence represents a mouse sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from an 8.5-day post coitum mouse library. Probes and primers derived from the sonic hedgehog may be used as diagnostic agents for neuromuscular, autonomic
                                                               Claim
                                                                                                             WPI; 95-255060/33.
N-PSDB; Q91637.
                                                                                                                                       30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD) HARVARD COLLEGE.
(IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
                                                                                                                                                                                                                                                                                                                                              08-MAR-1996 (first entry)
Mouse sonic hedgehog protein.
Mouse; sonic hedgehog protein;
nervous system disorder; gene t
                                                                                      Hedgehog-like protein(s)
to treat degenerative nea
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13-JUL-1995.
                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRV
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                                                               17; Page 139-41; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                        /note=
279
                                                                                                                                                                                                                                                                                 /note= "signal peptide'
25. .30
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.8%;
61.1%;
                                                                                        nervous
                                                                                                                                                                                                                                            "N-linked
                                                                                                                                                                                                                                                                    "conserved sequence (R77349)"
                                                                                     and nucleic rvous system
                                                                                                                                                                                                                                                                                                                                              otein; probe; primer; diagnostic;
gene therapy; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AWGSWTPGEGVHWYPQLLYRLGRLLLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1279.5; DE Pred. No. 3e-122;
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disorder(s)
                                                                                      encoding
er(s) and i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              central nervous system disorders, and the gene may also be used gene therapy. Antibodies generated from the protein may be used
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                                                                                                                                                                                                                                                                                                                                       KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
ETMHPLGMA
                      GSFHPLGMS
                                                                             LRLFHSL----
                                                                                                                       VPG----LQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP
                                                                                                                                                                           VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR
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                                                   FRLAHALLAALAPARTDGGGGGSIPAAQSATEARGA-EPTAGIHWYSQLLYHIGTWLLDS
                                                                                                      ERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSWAHRAFAP
                                                                                                                                                         DEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQRVYVVA
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                                                                                                                                                                                                                                                                                                                       KITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVRLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                   261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or research reagents. AA;
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60.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1276.5; DE Pred. No. 6e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                           -AWGSWTPGEGVHWYPQLLYRLGRLLLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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RESULT 11
W94471 standard; Protein; 437 AA.

RC W94471;
DT 29-APR-1999 (first entry)
DT 29-APR-1999 (first entry)
DE Mouse Shh hedgehog proteins sequence.
KW Patched; hedgehog; ptc therapeutlc; neuroprotective; neuronal cell;
KW Patched; hedgehog; ptc therapeutlc; neuroprotective; neuronal cell;
KW Drain infarction; cerebral infarction; transient ischaemic attack;
KW brain infarction; cerebral infarction; transient ischaemic trauma;
KW brain infarction; cerebral infarction; transient sedema; trauma;
KW brain infarction; cerebral infarction; spinal cord; oedema; trauma;
KW brain infarction; cerebral infarction caused by ischaemic or epoxic productions of the treatment and prevention of e.g.
PR 27-JUN-1997; US-883656.
PA (ONTO-) ONTOGENY INC.
PA Nahanthappa NK;
PR N-PSDB; X16185.
PT Wethod for limiting damage to neurons caused by ischaemic or epoxic conditions of the treatment and prevention of e.g.
PT conditions - is used for the treatment and prevention of e.g.
PT conditions - is used for the treatment and prevention of e.g.
PT conditions - is used for the transient ischaemic attacks
PS Disclosure; Page 68-70; 104pp; English.
CC ischaemic or epoxic conditions by administering a ptc (patched)
CC ischaemic or epoxic conditions by administering a gane activation construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a gene. Administration of the ptc therapeutic agent is used to protect
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W97768
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Best Local Similarity
Matches 261; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The present sequence represents a hedgehog sequence given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Sonic hedgehog (Shh) protein.
Sonic hedgehog; Shh protein; mouse; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's dis
Huntington's disease; amyotrophic lateral sclerosis;
Increasing the survival of neuronal, dopaminergic and GABA cells - by using a ptc therapeutic such as a protein kinas inhibitor, or an agent derived from hedgehog polypeptides,
                                                                                                                                                                                                                                        04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
                                                                                                           N-PSDB; X07274.
                                                                                                                                          WPI; 99-142578/12.
                                                                                                                                                                      (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, Pang
                                                                                                                                                                                                                                                                                                                                            WO9904775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              hypoxia;
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                                         dopaminergic and GABA-nergic
uch as a protein kinase
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             useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
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Disclosure; Page 89-91; 138pp; English.
This polypeptide is mouse Shh Sonic hedgehog protein. The
invention is based on the finding that hedgehog proteins are useful
as protective agents in the treatment and prophylaxis of
neurodegenerative disorders resulting from the loss of dopaminergic
and/or GABA-nergic neurons, or the general loss of tissue from the
substantia nigra. Exemplary disorders include Parkinson's disease,
Huntington's disease (both claimed), amyotrophic lateral sclerosis
and cerebral ischaemia. The invention relates to hedgehog
therapeutics (i.e. hedgehog polypeptides and gene therapy constructs
e.g. constructs encoding recombinant hedgehog gene regulatory
ctrans-activation constructs for altering hedgehog gene regulatory
sequences) and ptc therapeutics (i.e. agents which mimic the effect
of naturally occurring hedgehog proteins on patched signalling)
that are effective in both human and animal subjects. Human Ihh
and Dhh polypeptides (see w97763-64) are preferred. The products
can also be used for the maintenance of differentiated neurons in
cultures, and to enhance the implantation of such neuronal cells in
an animal. They can be used to prevent or treat neurodegenerative
conditions arising from the use of certain drugs, and ip the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 261
              Mouse Sonic hedgehog protein Shh. sonic hedgehog; Shh protein; mouse; hedgehog therapeutic; ptc therapeutic; patched; signal transduction; muscle atreachexia; muscular myopathy; myoblastic sarcoma; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.
                                                                                     Y05513;
05-JUL-1999
                                                                                                                   Y05513 standard; Protein; 437
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                                                                                                                                                                                                                                                                                                                KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
                                                                                                                                                                                                            ETMHPLGMA 433
                                                                                                                                                                                                                                                                                                                                                                      VPG----LQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP
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                                                                                      (first entry)
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                                muscle atrophy;
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PS Disclosure; Page 115-116; 130pp; English.
CC The present sequence is mouse Sonic hedgehog protein Shh. The
CC invention relates to a method for modulating the formation and/or
CC maintenance of muscle tissue by ecotopically contacting muscle
CC cells, especially muscle stemp/progenitor cells, in vitro or in
CC vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and
CC gene therapy constructs) or ptc therapeutic (i.e. a small organic
CC molecule that mimics the effect of hedgehog proteins on patched
CC signalling, or activates or potentiates patched signalling) in an
CC amount effective to alter the growth state of the treated cells.
CC also claimed is a method for treatment or prevention of disorders
CC of, or surgical or cosmetic repair of, such muscle tissues, by
CC administering a hedgehog polypeptide or ptc therapeutic. The
CC disorder may be muscle atrophy, in particular skeletal muscle
CC atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy
CC (all claimed). The hedgehog polypeptide or ptc therapeutic can
CC inhibit growth of myoblastic derived tissue to provide treatment of
CC myoblastic sarcoma (also claimed). The hedgehog therapeutic
CC myoblastic sarcoma (also claimed). The hedgehog therapeutic
CC preferably comprises at least a bioactive extracellular portion of
CC genence (see x2598-107), especially a human hedgehog gene.
CC Genence
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Best Local
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Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
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04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVRLRV
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                                                                                                          GSFHPLGMS 407
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nilarity 60.8%;
Conservative 4
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Pred. No. 6e-122;
0; Mismatches 91;
                                                                                                                                                                                -----AWGSWTPGEGVHWYPQLLYRLGRLLLEE 398
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PS Claim 13: Pages 150-151; 210pp; English

CC This represents a zebrafish sonic hedgehog (shh) protein sequence. The

CC differention provides methods and compounds for modulating proliferation or

CC differentiation of neuronal cells, cholesterol biosynthesis or transport

CC or expression of pituitary gland genes. The method for affecting

CC cholesterol biosynthesis or transport in a cell comprises contacting a

CC cell with a compound that affects hedgehog, thereby affecting cholesterol

CC biosynthesis or transport. The methods for inhibiting the neural inducing

CC cellyty of a hedgehog polypeptide in cells, and for inducing pituitary

CC gland gene expression utilises sequences selected from a zebrafish

CC tiggy-winkle hedgehog (twhh) protein (W61487) or a mouse shh

CC (shh) protein (W61486), a chicken shh protein (W61487) or a mouse shh

CC can affect hedgehog activity. They can be used for treating disorders

CC which arise from neuronal degeneration or abnormal function. They can

CC also be used as nerve-sparing agents or in restoring or promoting

CC appropriate patterning during the healing of major limb trauma. They can

CC also be used for treating Smith-Lemli-Optiz syndrome. The products can

CC convence A 18 a.
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Best Local Similarity
Matches 254; Conserv
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07-OCT-1996; US-709743.
07-OCT-1996; US-709743.
(UYJO) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
Beachy PA, Porter JA;
Wer; 98-399053/34.
New hedgehog-derived poly:peptide(s) - used to develop products for modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
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Hedgehog polypeptide; neuronal cell proliferation; zebrafish;
cholesterol biosynthesis; pituitary gland gene expression; shh;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
neuronal degeneration; nerve-sparing agent; Smith-Lemil-Optiz syndrome.
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20-OCT-1998 (first entry)
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364 LRLFH---
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                                                                                                                                                              VKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLRPRLHFCLVLLLLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGAS
                                                                                                                                                                                                                                               HVHCSVKSEHSAAAKTGGCEPAGAQVKLESGARVALSAVRPGDRVLAMGEDGSPTFSDVL
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                                                           MVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFAP
                                                                                                     LVAGVPG
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                                                                                                                                         MFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQKV
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  -SLAWGSWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMS
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Pred. No. 1e-121;
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Best Local Similarity
Matches 267; Conserv
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30-DEC-1994; US-176427.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Momahon AP, Tabin CJ;
WPI; 95-255060/33.
N-PSUB; 091639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy.

Claim 17; Page 143-45; 210pp; English.

The sequence represents a human sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDN/ isolated from a human fetal lung cDNA library. Probes and primers isolated from the sonic hedgehog gene may be used as diagnostic derived from the sonic hedgehog gene may be used as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sonic hedgehog protein.
Human; sonic hedgehog protein; probe; primer; diagnostic;
nervous system disorder; gene therapy; antibody.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R77341;
14-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hedgehog-like protein(s) and nucleic acid(s) encoding them to treat degenerative nervous system disorder(s) and in gene
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VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                      PHRLRAFQVIETQDPPRRLALTPAHLLFTA---DNHT-EPAARF-------RATF 294
                                                                                                                                                                      KAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRD
                                                                                                                                                                                       KSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDRE 250
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                                                                                                                                                                                                                                                                                                                                                     AVADHHLAQLAFWPLRLFHSL------
                                                                                                                  DGAKKVFYVIETREPBERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF
                                                                                                                                                                                                                                    EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV
                                                                                                                                                                                                                                                                                             ISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVT
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                                                                                                                                                                                                                                                                                                                                                                                                              58.4%; Score 1271; DB 1; 57.7%; Pred. No. 2.5e-121; tive 45; Mismatches 85;
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Search completed: June 5, 2000, 08:16:18 Job time: 2583 sec

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Result
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/cOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-176-427B-6
US-08-356-060A-10
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US-08-356-060A-14
PCT-US95-15463-20
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-8
US-08-356-060A-8
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US-08-356-060A-12
PCT-US95-15463-17
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PCT-US95-15463-19
US-08-356-060A-9
US-08-356-060A-9
US-08-356-060A-40
US-08-356-060A-41
US-08-356-060A-41
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US-08-356-060A-41
US-08-356-060A-43
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                             Sequence 6, Appli Sequence 11, Appl Sequence 20, Appl Sequence 21, Appl Sequence 11, Appl Sequence 11, Appl Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli Sequence 17, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Seq
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136 DGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHS 195

ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDE 135

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76 \vdash

Hest Local Similarity 94.98;
Matches 319; Conservation

Score 1686; DB 1; Pred. No. 2.1e-168; 9; Mismatches 8;

Length 336; Indels

0;

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RESULT 1 (US-08-176-427B-6 (U	30 346 15.9 73 1 US-08-176-427B-12 31 346 15.9 73 2 US-08-356-060A-35 32 315 14.5 64 1 US-08-176-427B-15 33 315 14.4 64 2 US-08-356-060A-17 35 314 14.4 64 2 US-08-356-060A-17 35 314 14.4 64 2 US-08-356-060A-17 36 300.5 13.8 65 1 US-08-176-427B-16 37 300.5 13.8 65 2 US-08-176-427B-16 38 263 12.1 64 2 US-08-356-060A-17 40 167 7.7 30 1 US-08-178-851-3 41 164 7.5 30 1 US-08-748-591-2 42 147 6.8 30 1 US-08-748-591-2 43 145 6.7 27 1 US-08-748-591-7 45 128 5.9 27 1 US-08-748-591-6
reto	Sequence 12, Appl Sequence 35, Appl Sequence 15, Appl Sequence 17, Appl Sequence 17, Appl Sequence 16, Appl Sequence 14, Appl Sequence 14, Appl Sequence 37, Appl Sequence 2, Appl Sequence 2, Appl Sequence 7, Appl Sequence 7, Appl Sequence 6, Appli Sequence 6, Appli

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-356-060A-10
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US-08-356-060A-10
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                                                            Query Match
Best Local Similarity
Matches 319; Conserv
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                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VIncent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-941
TELEPHONE: (617) 227-941
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION MATE: US/08/356,060
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALUMAN, COUNTRY: BOSTON STATE: MA COUNTRY: USA COUNTRY: USA COUNTRY: O2109
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                 ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDE 135
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                                                               Conservative
                                                                                                                                                                          linear
                                                                                                                                                       protein
                                                                          77.5%;
94.9%;
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                                                                                                                                                                                                                                                                                                  HMI-006CP
                                                                            Score 1686; DB 2;
Pred. No. 2.1e-168;
                                                             9:
                                                             Mismatches
                                                                                          Length 336;
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                                                            0;
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101 RLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDR 160

Query Match
Best Local Similarity
Matches 311; Conserv

75.7%; Score 1646; DB 2; ilarity 100.0%; Pred. No. 2.8e-164; Conservative 0; Mismatches 0;

Length 313;

0;

Gaps

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RESULT 3
US-08-356-060A-14
; Sequence 14, Application US/08356060A
; Patent No. 5844079
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US-08-356-060A-14
                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            COMPUTER: IBM_PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427
APPLICATION NUMBER: US/08/176,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: Michahon, Andrew P.
APPLICANT: Tabin, Clifford J.
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                       FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TPSEGVHSYPQMLYRLGRLLLEESTFHPLGMSGAGS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 RVAAVSTHVALGAYAPLIKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAWGSW 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPGLQPA
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                                          LENGTH: 313 amino acids
TYPE: amino acid
TODOT
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ZIP: 02109
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14-DEC-1994
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PCT-US95-15463-20
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                                                                                                                 Best Local Similarity
Matches 262; Conserv
                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                            TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
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                                                                                                                                                                                                              MOLECULE TYPE: protein
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/15463 FILING DATE: 01-DEC-1995 CLASSIFICATION:
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70 KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
                                                                     13 CLVLLL----LLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG 69
                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
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                                                  FHPLGMSGAGS 411
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                                                                                                                                58.8%;
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                                                                                                                 39; Mismatches
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                                                                                                               Score 1279.5; DB 4;
Pred. No. 1.2e-125;
39; Mismatches 91;
                                                                                                                 Indels 37;
                                                                                                                                                 Length 437;
                                                                                                                 Gaps
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PCT-US95-15923-20
; Sequence 20, Application PC/TUS9515923
; GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine,
ITILE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
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                                                                             Query Match 58.8
Best Local Similarity 61.1
Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
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                       13 CLVLLL----LLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG 69
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                                                                           58.8%; Score 1279.5; DB 4; 61.1%; Pred. No. 1.2e-125; vative 39; Mismatches 91;
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US-08-176-427B-8
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                                                                       TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                  FILING DATE: 30-DEC-1933
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REFISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,4:
FILING DATE: 30-DEC-1993
              TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD
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STREET:
STREET:
BOSTON
WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 02109
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                                                        amino acid
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GENERAL INFORMATION:
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Best Local Similarity
                APPLICATION NUMBER: US 08/176,427
ETLING DATE: 30-DEC-1993
ATTORNEY_AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060.
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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(617) 227-7400
                                                                                                                                                                                                                                                                                                          Floppy disk
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Pred. No. 2.4e-125;
Pred. No. 2.4e-125;
                                    HMI-006CP
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-356-060A-11
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PCT-US95-15463-18
                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application PC/TUS9515463
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
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                                                                COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15463
FILING DATE: 01-DEC-1995
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETMHPLGMA 433
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:: CA
                                                                                                                                                                                                                                                                                     E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400
 38,347
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application PC/TUS9515923
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine,
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.6%; Score 1274; DB 4; Best Local Similarity 61.2%; Pred. No. 4.1e-125;
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                                                                                CURRENT APPLICATION NUMBER: PCT/US95/1500 FILING DATE: 04-DFC CLASSIFT.
                                                                                                                                                                                 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 HVHCSVKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 MVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 ARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLLDSNMLHPLGMS
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                                                                                                                                                                                                                                                                                                                               STREET: 4225 EX CITY: La Jolla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLLTRVLLVSLLTLSLVV-SGLACGPGRGYG-RRRHPKKLTPLAYKQFIPNVAEKTLGAS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKLRVTEGWDEDGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDFI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP 363
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                                                                                                                                                                                                                                                                                                             CA
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                                                                                                                                                                                                                                                                                                                                                           Square, Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07265/080WOI
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07265/043WO1

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; LENGTH: 418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-15923-18
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US-08-356-060A-13
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Best Local Similarity 61.2%;
Matches 254; Conservative 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
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                                                                                                                                                                                                     CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP 363
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                                                                                                                                                                                        02109
                                                                                                                                                                                                                                                                     60 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 14;
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Sequence 2, Application US/08176427B Patent No. 5789543

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.

Ingham, Phillip W.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

STREET: CITY: I

60 State Street

LAHIVE & COCKFIELD

ADDRESSEE:

COUNTRY: UZIP: 02109

: Boston E: MA TRY: USA

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US-08-176-427B-2
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                       RESULT 11
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 30-DEC-1993 ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P.
                                                                         379 ----EGVHWYPQLLYRLGRLLLEEGSFHPLGMS------GAG 410
|:||| ||||::| ||: :|||||:
426 AGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAG 468
                                                                                                                                                                                                                           306 ASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYA
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                                                                                                                                                   366 VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                                                                                                                                                       13 CLVLLLL--LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
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les 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 475 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CLLLVLVSSLLVCSGLACGPGRGFG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK 65
                                                                                                                                                                                                                                                ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                                                                                                                                                                                                     DGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF 305
                                                                                                                                                                                                                                                                                                                                                                              KAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.4%; Score 1271; DB 2; 57.7%; Pred. No. 1e-124; ative 45; Mismatches 85;
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US-08-356-060A-8
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TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08356060A Patent No. 5844079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.0 Matches 257; Conservative
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                                                                                              GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: Michahon, Andrew P.
APPLICANT: Michahon, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
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FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,709
REFERENCE/OCCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      378
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STREET:
CITY: E
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IETQDPPRRLALTPAHLLFTADNHTEPAA----RFRATFASHVQPGQYVLVAGVPGLQ-- 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVSSGLTCGPGRGIG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGKITRNSERFK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEHSWAHWAFAPFRLAQGLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IETROPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASNVKPGQRVYVLGEGGQQLL 317
                      60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.4%; Score 1270.5; DB 1; 63.0%; Pred. No. 9.7e-125; ative 38; Mismatches 96;
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APPLICANT:
APPLICANT:

APPLICANT: Epstein, Ervin APPLICANT: Hu, Zhilan APPLICANT: Bonifas, Jeanette TITLE OF INVENTION: Mutant Human Hedgehog Gene

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US-08-748-591-4; Sequence 4, Application US/08748591; Patent No. 5759811; Patent No. 5759810; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,01
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                    138
                                                                                                                              378 ALCPDGAIPTAATTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS
                                                                                                                                                                                                                                    314 PARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAW 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                    PASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEHSWAHWAFAPFRLAQGLLA
                                                                                                                                                                                                                                                                                                                                                                                 TGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASNVKPGQRVYVLGEGGQQLL
                                                                                                                                                                                                                                                                                                                                               SGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLTFLDRMDSSRKLFYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLVSSGLTCGPGRGIG-KRRHPKKLTPLAYKOFIPNVAEKTLGASGRYEGKITRNSERFK 77
                                                                                                                                                                                                                                                                                                          IETQDPPRRLALTPAHLLFTADNHTEPAA----RFRATFASHVQPGQYVLVAGVPGLQ--
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NUMBER OF SEQUENCES:

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 854-0875 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                        246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSV 190
                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                              186
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                                                                             426 AGATAGIHWYSQLLYQIGTWLLDSEALHPLGMA 458
                                                                                                                                                        366 VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGDRGGGGGRVALTAPGAADAPG
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 CLLLVLVSSLLVCSGLACGPGRGFG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVT 130
                                                                                               ----EGVHWYPQLLYRLGRLLLEEGSFHPLGMS 407
                                                                                                                                                                                                                               ASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYA
                                                                                                                                                                                                                                                                   ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                                                                                                                                                                                                        DGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV 185
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Patent No. 5759811
GENERAL INFORMATION:
APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Hu, Zhilan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.3%; Score 1268.5; DB 1; Best Local Similarity 58.3%; Pred. No. 1.8e-124; Matches 264; Conservative 45; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Fish and
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TITLE OF INVENTION: Mutant Human Hedgehog
NUMBER OF SEQUENCES: 23
                                      350 AVADHHLAQLAFWPLRLFHSL------
                                                                                                                                                                                                                                  126 EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV
                                                                                                                                                                                                                                                                                                                                      131 EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSV 190
366 VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                                                                                   295 ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                                                         246 DGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/748,591 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 CLVLLLL--LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Menlo Park
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CLLLVLVSSLLVCSGLACGPGRGFG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK 65
                                                                                                                                                                                              PHRLRAFQVIETQDPPRRLALTPAHLLFTA---DNHT-EPAARF------RATF
                                                                            ASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAXAPLTAQGTILINRVLASCYA
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PCT-US95-02315-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: JOHN P. WHILE
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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246 DEGAKKVFYVIETREPRERLLITAAHLLEVAPHNDSGPTPGPSPLFASRVRPGQRVYVVA 305
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ZIP: 10036
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                           EPHRLRAFQVIETQDPPRRLALIPAHLLFTA-DNHTEPAARFRATFASHVQPGQYVLVAG 308
                                                                                                          VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
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                                                                         VKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDR 245
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Edlund, Thomas
Edlund, Thomas
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AVENTION: HEDGEHOG, VHH-1, EXPRESSED BY THE NOTOCHORD, AND USES
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                                                                 FRIAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPA-GIHWYSQLLYHIGTWLLDS
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Search completed: June Job time: 1299 sec 5 2000, 08:17:15

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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C49425
C;Species: Mus musculus (house mouse)
C;Decies: Musculus (house mouse)
C;Decies: Mullor: Shen, L.; Mohler, J.; McMahon, J.A.; M
Ccll 75, 1417-1430, 1993
R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; M
Ccll 75, 1417-1430, 1993
R;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is imp
A;Accession: C49425
A;Accession: C49425
A;Cross-references: A49425; MUID:94094334
A;Residues: 1-336 <ECH>
A;Cross-references: GB:X76291
RESULT 2.

A49425

A49425

Sonic hedgehog protein precursor - mouse
C:Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: A49425
C;Epstein, D.J.; St-Jacques, B.: Shon T. Wohlow T. Woh
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Pred. No. 1.
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       J.; McMahon,
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Gaps

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RESULT 8
B49425
Desert hedgehog protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: B49425
C:Accession: B49425
C:Accession: B49425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A. Cell 75, 1417-1430, 1993
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is A;Reference number: A49425; MUID:94094334
A;Accession: B49425
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A;Molecule type: DNA
A;Residus: 1-396 <ECH>
A;Cross-references: GB:X76292;
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                                                                                                                                                                                                                                     PARLRPRLHFCLVLLLLLVVPAAMGCGFGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVLAPGGDALQPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAF
               QYVLVAGVPGLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAF
                                                                        DVLIFLDREPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPG
                                                                                                                                              SKAHVHCSVKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFS
                                                                                                                                                                             WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYE
                                                                                                                                                                                                                                                                                              PASILPIC -- CLALLAL ---- SAQSCGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRLFH--SLAWGSWTPGEGVHWYPQLLY------RLGRLLLEEGSFHPLGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METDRDSTTRRVEYVIETQEPVEKITLTAAHLLEVLDNSTEDLHTMTAAYASSVRAGQKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVHCSVKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVL
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                                                                                                                    SRNHIHVSVKADNSLAVRAGGCFPGNATVRLRSGERKGLRELHRGDWVLAADAAGRVVPT
                                                                                                                                                                                                                                                                                                                                                        Similarity 58.
                                                                                                                                                                                                                                                                                                                                                                                                                            sonic hedgehog
                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 1175; DB 2; 58.5%; Pred. No. 5.5e-92; tive 50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g443941;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 396;
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                                                                                                                                                                                                                                                                                                     C;Superfamily: sonic hedgehog protein
C;Keywords: transmembrane protein
F;62-82/Domain: transmembrane #status predicted <TMM>
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A:Introns: 160/3; 248/1
C:Superfamily: sonic hedgehog protein
C:Keywords: transmembrane protein
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A; Gene: hh
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A; Residues: 1-471 <LEE>
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A;Molecule type: mRNA
A;Residues: 1-471 <TAB>
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                                                                                                                                                                                                                                   Query Match 41.1%; Score 893.5; DB 2; Best Local Similarity 45.9%; Pred. No. 5.3e-68; Matches 189; Conservative 61; Mismatches 131;
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N; Alternate names: hh protein
C:Species: Drosophila melanogaster
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C:Accession: A46400; JNO501; A43480
R; Tabata, T; Eaton, S; Kornberg, T.B.
Genes Dev. 6, 2635-2645, 1992
A; Title: The Drosophila hedgehog gene is expressed specifically in posterior A; Reference number: A46400; MUID:94040725
A; Reference number: A46400; MUID:94040725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-471 <TAS:
A; Cross references: GB:L05404
A; Note: it is uncertain whether Met-1 or Met-51 is the initiator
A; Note: intron positions were determined from partial DNA sequence
R; Lee, JJ; yon Kessler, D.P.; Parks, S.; Beachy, P.A.
Cell 71, 33-50, 1992
Cell 71, 33-50, 1992
A; Title: Secretion and localized transcription suggest a role in pc
A; Accession: A43480
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A;Experimental source: Oregon-R
A;Experimental source: Oregon-R
A;Note: sequence extracted from NCBI backbone (NCBIN:138996, NCBIP:138997)
R;Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, F.;
Gene 124, 183-189, 1993
A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene rec
A;Reference number: JNO501; MUID:93185922
A;Accession: JNO501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L02793; NID:g157609; PID:g157610
A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
C;Comment: This protein is required for cell-cell communicat
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                                                                                                                                                                                    130 TEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCS
                                                                  190 VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
                                                                                                                                                                                                                                                                                                   125 VIRRDSPKFKDLVPNYNRDILFRDEEGTGADRLMSKRCKEKLNVLAYSVMNEWPGIRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LVLLLLLVVP----AAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG
VKSDSSISSHVHGCFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDR 304
                                                                                                                                                                                                                                                                                                                                          KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV
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A; Nolecule type: DNA
A; Residues: 1-615 < NHA>
A; Residues: 1-615 < NHA>
A; Cross-references: EMBL: U88183; PIDN: AAB52656.1; GSPDB: GN00028; CESP: ZK377.1
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A; Introns: 46/1; 70/3; 157/2; 176/1; 245/2; 314/3; 402/3; 499/2
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A; Reference number: Z20639
A; Accession: T29550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-94 <DRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: H01643
A; Accession: G02735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: G02735 R;Drummond, I.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             desert hedgehog - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                               A; Gene: CESP: ZK377.1
                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZK377.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Caenorhabditis elegans;Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
342 QSGSYSGSYSGYPTADASQYNAYPAMQQPAYQPAYQPAYQPAYQPAYQPAYQPAYQPAYSARGY 401
                                  142 ESLHYEGRAVDITTSDRDR-NKYGLLARLAVEAGFDWVYYES-KAHVHCSVKSEHSAAAK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 RAVDITTSDRDRNKYGLLARLAVEAGFDWVYYES 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 STLE--AWLPAKEQLHSSPKVVSSAQQQNGIHWYANALYKVKDYVLPQSWRH 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 HSLAWGSWTPGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 EPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGV
                                                                     Local Similarity 24.7
les 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLEQMQNFVQLHT-DGGAVLTVTPAHLVSVWQPESQ---KLTFVFADRIEEKNQVLVRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETGELRPQRVVKVGSVRSKGVVAPLTREGTIVVNSVAASCYAVINSQSLAHWGLAPMRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                    8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.0%;
                                                                     52;
                                                                    Score 174.5; DB 2
Pred. No. 7.6e-07;
2; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 456; DB 2; Pred. No. 7.6e-32;
                                                                                                                                                                                                                                                                                                      from
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                                                                                                     DB 2;
                                                                    111;
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A; Molecule type: DNA A; Residues: 1-1021 <WIL>

GB/EMBL/DDBJ

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submitted to the EMBL Data Library
A;Reference number: Z19716
A;Accession: T23752
A;Status: preliminary; translated
                                                                                                                                                                                                                         RESULT
T23252
                                                                                                                          hypothetical protein K02E2.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T23252
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A; Introns: 45/3; 200/1; 235/3; 436/3; 561/3; 581/3; 696/3; 742/1; 826/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-868 <WIL>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ainscough, R.
submitted to the EMBL Data
A;Reference number: Z19541
A;Accession: T22281
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                        R;Lloyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571 SLYKRTSSVFHNLMFFKSSTEEG
                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                   ROKVLNLFGILHMNEIELPTGTAVYKELL 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETQDPPRRLALTPAHLLFTA-------DNHTEPAARFRATFASHVQPGQYVLVA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCFSSDTLVTTPSGKK-RMDEIDVGDYVLTANR-VKTHFTPVTLWIHRESEKLEEFLTI 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PL----RLFHSLAWGSWTPGEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTE-----PAARFRATFASHVQPGQ 302
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                                                                                                                                                                                                                                                                                                                                                                                                             ENTKFRQEKINQTTRGLKTGIYSPLTKNGRIIVNDMLASCYSEVQANVLQTTYFWVFNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPGLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TTERGSTLQLTPLHFMYRTKCNESSEFLKILPENH-----EAILASYLEIGDCVILT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 26.3
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: 281540; PIDN: CAB04405.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 173.5; DB 2;
26.3%; Pred. No. 1.5e-06;
Live 33; Mismatches 90;
                                                                              Library,
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                                                                                November
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hypothetical protein T05C12.10 - Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T23754; T24513
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T23754
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A; Residues: 1-1226 <WIL>
A; Cross-references: EMBL: 268008; PIDN: CAA92000.1; GSPDB: GN00028; CESP: R08B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1995 A; Reference number: Z19834 A; Accession: T24045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; White, S.
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Best Local Similarity 24.3%; Pred. No. 3.3e-06;
Matches 55; Conservative 42; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
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                                                                                                                                                                                                           1133 KYRQQKIETITRSVRTGIYSPLTNNGRIIVNDMLASCYSEIQQNTLQTTFFW 1184
                                                                                                                                                                                                                                                                                                                   1074
                                                                                                                                                                                                                                                                                                                                                                                                                 1016 AATGACFSLDTWVTTPTGKK-RMDQIDIGDYVLTADLE-KTYFTPITLWIHREPEKVQEF 1073
                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 AKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAF 257
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Local Similarity 25.0%; Pred. No. 2.7e-05;
hes 43; Conservative 39; Mismatches 80; Indels 1
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INDIAN HEDGEHOG PROTEIN C.-PRODUCT.
INDIAN HEDGEHOG PROTEIN C.-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (
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P97812; Q61724;
15-JUL-1999 (Rel.
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15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                               AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARAPHYROID HORMONE-RELATED PROTEIN (FPHRP).

OF PARAPHYROID HORMONE-RELATED PROTEIN EXPRESSION WITH THE CELL SURFACE. IS ALSO SECRETED IN ETHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OPHER CELLS (BY SIMILARITY).

OF MEDIATE SIGNALING TO OPHER CELLS (BY SIMILARITY).

OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM AND UNGCENITAL SINUS. IN THE ADULT KLDNEY, FOUND IN PROXIMAL CONVOLUTED AND PROXIMAL STRAIGHT TUBULE.

OEVELOPING GUT, AT 14.5 DAYS DOC IN THE CARTILAGE PRIMORDIUM AND IN THE DEVELOPING UNCCENTRAL SINUS. EXPRESSION INCREASES WITH GESTIONAL AGE IN KIDNEY AND DUDDENUM, BECOMING MAXIMAL IN GESTIONAL AGE IN KIDNEY AND DUDDENUM, BECOMING MAXIMAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity."; Cell 75:1417-1430(1993).
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Zhao R., Seldin M.F., Fallon J.F., Beachy
"Products, genetic linkage and limb patter
hedgehog gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dressler G., Holzman L.B.;
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MEDLINE; 97236802.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY),

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURRING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE DETWEEN GROWTH
SWISS-PROT entry is copyright.
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Beachy P.A.;
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PRINTS; PR00632; SONICHHOG
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EMBL; X76291; CAA53923.1; -.
MGD; MGI:96533; IHH.
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PROTEIN PRECURSOR (IHH)
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RI and PTH-related protein.";

RI Science 273:613-622(1996).

CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EYENTOMS IN ASSOCIATION WITH SMOOTHENED (SMO), TO CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED IN CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN CC AND OSSIFICATION: THE DEVELOPING BONES. INDUCES THE EXPRESSION CC OF PARATHYROLD HORMONE-RELATED PROTEIN (PTHRP).

CC -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM CC TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND CC CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.

CC -!- FIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY OF THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TENTINAL OF THE NEWLY GENERATED N-CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CC ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CC SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.

CC -!- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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commercial
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CHAIN CHAIN CHAIN SITE SITE SITE Signal. EMBL; U58511; AAC60010.1; -. PFAM; PF01079; Hint; 1. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ACT_SITE PRINTS; PFAM; PF01085; HH_signal; 1. Developmental PR00632; 1 24 24 199 198 244 271 protein; SONICHHOG 23 408 198 408 199 244 271 268 Autocatalytic cleavage; INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER () SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE SIMILARITY). ESSENTIAL SIMILARITY) FOR AUTO-CLEAVAGE Hydrolase; (BY

밁 Ş Q. Query Match Best Local S Matches 320 61 4 _ MSPARLRPRLHFCLVLLLLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKT 60 LGASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMN MKPARLLLLLSGC----ALLLAPAVRCCGPGRVVGSRRRPPRKLIPLAYKQFSPNVPEKT Similarity 75.7%;
nilarity 77.7%;
Conservative 2: 21; Score 1645.5; DB 1; Pred. No. 7.8e-131; 1; Mismatches 66; Indels Length 408; ហ Gaps 56

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M.

CHOLESTEROL (BY SIMILARITY).
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Q91612;
15-JUL-1999
15-JUL-1999
                                                                  This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (BA
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Xenopodinae;
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062226;
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15-JUL-1999 (Rel. 38, La
SONIC HEDGEHOG PROTEIN P
SHH OR HHG1.
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DOMAIN
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO:
                                                       Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                           Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKVVLLLCAAALLLSGAVRGCGPGRVVGRRRR-PTKLSPLSYKQFSPNVPEKTLGASGRY 62
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285; Conservative
                                           Rodentia;
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                                                                                                                                                                        STANDARD;
                                                                                                             38, Created)
38, Last sequence up
38, Last annotation
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                                       Chordata; Craniata;
Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.2%;
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                                                                                                  PRECURSOR
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Pred. No. 3.5e
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN C-PRODUCT
INDIAN HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ARG
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ESSENTIAL FOR AUTO-CLEAVAGE
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                                                                                                  (SHH)
                                             Muridae;
                                                                                                               on update)
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ches 74;
                                                                                                  (HHG-1).
                                           Vertebrata;
ae; Murinae;
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                                                         Mammalia;
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-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.
-!- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.
-!- INDUCTION: BY RETINOID ACID:
-!- INDUCTION: BY RETINOID ACID:
-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACITVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL PRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVITY SOURCE AS NO SCIENTAL MORE SIGNALING, WHEREAS THE G-ENDICE AND LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T., Beachy P.A., Jessell T.M.;
"Floor plate and motor neuron induction by different concentrations the amino-terminal cleavage product of sonic hedgehog autoproteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sonic hedgehog, a member of a family of putative molecules, is implicated in the regulation of CNS Cell 75:1417-1430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall T.M.T., Porter J.A., Beachy P.A., Leahy D.J.;

"A potential catalytic site revealed by the 1.7-A crystal structure

"A potential signalling domain of Sonic hedgehog.";

Nature 378:212-216(1995).

-i- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMahon A.P.;
Submitted (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94094334.
Echelard Y., Epstein D.J., St Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 81:445-455(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang D.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. AN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NUBRAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NUBRON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
C-PRODUCT HAS NO SIGNALING ACTIVITY.
SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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R., Seldin M.F., Fallon J.F., Beac
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ation update) (SHH) (VHH-1).

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RESULT 6
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Best Local
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DOMAIN
SEQUENCE
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SIGNAL
SH_BRARE STANDARD; PRT; 4
92008; O13170; O13171;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
SONIC HEDGEHOG PROTEIN PRECURSOR (SHH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
CHAIN
CHAIN
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF01085; HH_signal; PRINTS; PR00632; SONICHHOG
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                                                                                                                                                                                                                                                                                EPHRLRAFQVIETQDPPRRLALTPAHLLFTA-DNHTEPAARFRATFASHVQPGQYVLVAG
                                                                                                                                                                                                                                                                                                                         VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR
                                                                                                                                                                                                                                                                                                                                                                                                                        KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
                                                                                                                    ETMHPLGMA
                                                                                                                                            GSFHPLGMS
                                                                                                                                                                  FRLAHALLAALAPARTDGGGGGSIPAAQSATEARGA-EPTAGIHWYSQLLYHIGTWLLDS
                                                                                                                                                                                           LRLFHSL----
                                                                                                                                                                                                                 ERGGDRRLLPAAVHSVTLREEEAGAVAPLTAHGTILINRVLASCYAVIEEHSWAHRAFAP
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383
437
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61.1%;
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Pred. No. 4.6e
39; Mismatches
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SONIC HEDGEHOG PROTEIN C-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR AUTO-CLEAVAGE
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1.6e-100;
1es 91;
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-I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE W-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SUBVACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-I- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN, ALSO FOUND IN THE OFTOCHORD AND IN DEVELOPING FIN BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DEWELOPING FIN INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON.

-I- DEVELOPMENTAL STAGES FIRST DETECTABLE IN THE INNER CELL LAYER OF THE EMBRYONIC SHIELD DURING GASTROLATION. BY 9.5 HRS OF THE DIENCEPHALON.

DEVELOPMENTAL STAGES FIRST DETECTABLE IN THE INNER CELL LAYER OF THE EMBRYONIC SHIELD DURING GASTROLATION. BY 9.5 HRS OF THE DIENCEPHALON. THE PRESUMPTIVE MIDBRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  closely related to the zebratish.;

Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

-: FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF ATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHI, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ekker S.C., Ungar A.R., Greenstein P
Moon R.T., Beachy P.A.;
"Patterning activities of vertebrate
developing eye and brain.";
Curr. Biol. 5:944-955(1995).
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Eukaryota; Metazoa; Chordata; Cranilata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fietz M.J., Concordet J.-P., Barbosa R., McMahon A.P., Tabin C., Ingham P.W.; "The hedgehog gene family in Drosophila Development Suppl. 43-51(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 96083328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roelink H., Augsburger A., Heemskerk J.,
Ruiz I Altaba A., Tanabe Y., Placzek M.,
Dodd J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EMBRYO;
MEDLINE; 94170375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zardoya R., Abouheif E.,
PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SCREACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
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Edlund
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, Jessell T.M.,
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Best Local Similarity
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360 ARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLLDSNMLHPLGMS
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                                                            LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP
                           LRLFH-----
                                                                                                                 IFLDREPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYV
                                                                                                                                                              HVHCSVKSEHSAAAKTGGCFFAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVL
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                                                HVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFAP
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                                                                                                 MFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQKV
                                                                                                                                                  HIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDFI
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S; PR00632; SONICHHOG
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SONIC HEDGEHOG PROTEIN N-PRODUCT.

SONIC HEDGEHOG PROTEIN C-PRODUCT.

SONIC HEDGEHOG PROTEIN C-PRODUCT.

CLEAVAGE (AUTO-).

INVOLVED IN CHOLESTEROL TRANSFER (1
                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                              Score 1274; DB 1;
Pred. No. 1.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                            HOLESTEROL (BY SIMILARITY).
CF000AFFFD2F5795 CRC64;
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Riddle R.D., Johnson .L., Laufer E., 1
"Sonic hedgehog mediates the polarizing
Cell 75:1401-1416(1993).
[2]
[2]
FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Noormathae: Galliformes; Phasianidae; Phasianinae; Gallus.
                                     Signal
SIGNAL
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Cell 81:445-455(19
-!- FUNCTION: BINE
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Floor plate and motor neuron induction by different concentrations the amino-terminal cleavage product of sonic hedgehog
                                                                                                         PFAM;
                                                                        Developmental
                                                                                                                                                                                                                                                                                                            C-PRODUCT HAS NO SIGNALING ACTIVITY.
SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                    L28099; AAA72428.1; -. PF01079; Hint; 1. PF01085; HH_signal; 1. S; PR00632; SONICHHOG.
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                                                                    protein;
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200
                                                                    Autocatalytic cleavage;
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ne polarizing activity
 POTENTIAL.
SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT
                                                                    Hydrolase;
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SHH_H
SHH_H
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Best Local
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                                                                                 Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T., Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.E., Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.; "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog."; Genomics 28:44-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                         SHH_HUMAN
Q15465;
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15-JUL-1999
15-JUL-1999
                 Strong C.,
Submitted
              SEQUENCE OF 1-187 FROM Strong C., Graves T., Submitted (AUG-1997) to
                                                                                                                                                                                  TISSUE-FETAL LUNG;
MEDLINE; 96070431.
                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                        Eukaryota;
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etazoa; Chordata; Craniata; Vertebrata; Mammalia;
imates; Catarrhini; Hominidae; Homo.
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to the EMB
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B; Mismatches
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                                 Ozersky
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2.6e-99;
ches 96;
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TSUI L.-C., Muenke M.;

"Mutations in the human Sonic Hedgehog gene cause holoprosencephaly.";

RL Nat. Genet. 14:357-350(1996).

C elenet. 14:357-350(1996).

C -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO). TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER ACTIVITY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL FOR A CONSTITUTIVE SIGNAL INDUCES DURING DEVELOPMENT: SIGNAL FOR A CONSTITUTIVE SIGNAL FROM THE NEURAL TUBE BY THE MOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE MEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE FLOOR PLATE-AND MOTOR NEURON INDUCTION IS CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS CONCENTRATION OF N-PRODUCT REQUIRED FOR FLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. SIGNAL FRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. SIGNAL FRESHOLD SIGNAL FROM INDUCTION (BY STATE DEVELOPING LIMB BUD. SIGNAL FROM INDUCTION
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1- DISCASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCASE: DISCASE THAT AFFECTS THE MIDLINE DEVELOPMENT OF THE FOREBRAIN AND MIDFACE. HPE IS ASSOCIATED WITH SEVERAL DISTINCT FACIES AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES, ANOPHTALMIA OR CYCLOPIA IS EVIDENT ALONG WITH A CONGENITAL DISSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEATURES FACIAL DISSOCIATED BY OCCULAR HYPERTELORISM, DEFECTS OF THE DISSOCRAFTS TO THE SECOND OF THE MIDLING CHARACTERIZED BY OCCULAR HYPERTELORISM, DEFECTS OF THE
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      EMBL; L38518; AAA62179.1; -. EMBL; AC002484; AAB67604.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORPUS CALLOSUM.
-!- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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Roessler E.,
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SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMLIARITY).

TISSUE SPECIFICITY: EXPRESSED IN FETAL INTESTINE, LIVER, LUNG, AND KIDNEY. NOT EXPRESSED IN ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR
Disease mutation.
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24 462
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   POTENTIAL.
SONIC HEDGEHOG PROTEIN.
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BINDING 197 197 CHO DOMAIN 407 411 POL DOMAIN 31 31 CHO VARIANT 117 117 FT VARIANT 117	CHAIN 24 CHAIN 198 SITE 197 SITE 243 SITE 267 ACT_SITE 270	CHAIN
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Anda CC and CLA Anda CC and CC	197 462 198 243 267 270	9
	SONIC HEDGEHOG PROTEIN N-PRODUCT. SONIC HEDGEHOG PROTEIN C-PRODUCT. CLEAVAGE (AUTO-) (BY SIMILARITY). INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY). INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).	OG PROTEIN N-PRODUC

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SIMILARITY).

CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR (BFGF) AND PORK HEAD.

(BFGF) AND PORK HEAD.

-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEDLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                     BINDING
SEQUENCE
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                                                                                                                                       LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIARSSERFK 79
                    SEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSVKSEHSAAAK 199
FEESLHYEGRAVDITTSDRDRSKYGMLARLAAEAGFDWVYFESKAHIHCSVKAENSVAAK 197
                                                                                         ELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHH 139
                                                                  ELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D63339; BAA09657.1; -. PF01079; Hint; 1. PF01085; HH_signal; 1. S; PR00632; SONICHHOG.
                                                                                                                                                                                                                               Similarity
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Biophys. Res. Commun. 218:395-401(1996).
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432 /
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268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                                                                                                               58.1%;
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                                                                                                                                                                                                                                                                                                     ₹.
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                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
SONIC HEDG
SONIC HEDG
SONIC HEDG
CLEAVAGE (
INVOLVED I
                                                                                                                                                                                                                               Score 1263; DB 1;
Pred. No. 1.1e-98;
                                                                                                                                                                                                                                                                                                                      CHOLESTEROL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                         ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                     B455C7E746C8E5A8 CRC64;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         HEDGEHOG PROTEIN.
HEDGEHOG PROTEIN N-PRODUCT.
HEDGEHOG PROTEIN C-PRODUCT.
HEDGEHOG PROTEIN C-PRODUCT.
AGE (AUTO-) (BY SIMILARITY).
VED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 head and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Protease;
                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeshima K.;
                                                                                                                                                                                                                                                                                                                                                         (BY
                                                                                                                                                                                                              28;
                                                                                                                                                                                                            Gaps
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RESULT 10
SHH_XEMA
ID 15-JU
DT 15
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SHLXENIA
SHLXENIA
(92000; Q91894;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation updat
15-FEB-2000 (Rel. 39, Last annotation updat
15-FEB-2000 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                      Ruiz I Altaba A., Jessell T.M., Roelink H.;

"Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";

MOL. Cell. Neurosci. 6:106-121(1995).

-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERWOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BLIDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHERIED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stolow M.A., Shi Y.-B.; "Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid hormone-dependent metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Distinct expression and shared gene family of Xenopus laevis."; Development 121:2337-2347(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ekker S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
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SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE W-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FOR MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: STONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION I OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

DEVELOPMENTAL STAGE: FIRST DETECTED AT THE NEURULA (STAGES 16-1
                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.T., Beachy P.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGRGLREATVERVYLEEATGAYAPVTAHGTVVIDRVLASCYAVIEEHSWAHWAFAPLRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IETQDPPRRLALTPAHLLFTADNH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHSLAWGSWTP----GEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a; Chordata; Craniata; Vertebrata;
Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23:2555-2562(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       С.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (X-SHH) (VHH-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TEPAARFRATFASHVQPGQYVLVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               members of the hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          von Kessler D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphibia;
      (STAGES 16-17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432
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Query Match
Best Local
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L39213; AAC42227.1; -.
EMBL; L39214; AAA85162.1; -.
EMBL; L35248; AAA49981.1; -.
PFAM; PF01079; H1nt; 1.
PFAM; PF01085; HH_signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                         127
        187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY THYROID HORMONE. PTM: THE C-TERMINAL DOMAIN DIS
                                                                                                                                                                                                                                                                          LLLL-----LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40). HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
KAENSVAAKSGGCFPAGARVMVEFGGTKAVKDLRPGDRVLSSDPQGNLLYSDFLMFIDQE
                                     KSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDRE 250
                                                                                EGWDEDGHHLEESLHYEGRAVDITTSDRDRSKYGMLGRLAVEAGFDWVYYESKAHIHCSV
                                                                                                      EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSV
                                                                                                                                                                                         IARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWFGVKLRVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORPHOGENESIS
                                                                                                                                                                                                                                                    LLLLSFICTLVTPPGLACGPGRGIG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK
                                                                                                                                                                   ITRNSDCFKELTPNYNPDIMFKDEESTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVT
                                                                                                                                                                                                                                                                                                                                                             Similarity
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394
403
                                                                                                                                                                                                                                                                                                                                           Conservative
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266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
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401
409
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Pred. No. 1.1e-97;
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TQSLL -> NSNLCW (IN REF. 3).
DPKTMTIKAKVEKVDLE -> ESQDHDLEGRGKWRRLILR
(IN REF. 3).
N -> S (IN REF. 3).
; 73B4B4932FA2EFF2 CRC64;
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                                                                            SIMILARITY)

-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSTERIOR LIMB BUD MESENCHYME.

-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics are no restrictions on in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHH_RAT
Q63673;
15-JUL-1999
15-JUL-1999
15-JUL-1999
SONIC HEDGEH
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Roelink H., Augsburger A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-EMBRYONIC FLOOR PLATE
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Eukaryota; Metazoa; Chor
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38, Last sequence update)
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Q90419;
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PF01085; HH_signal; 1.
PF01085; SONICHHOG.
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C HEDGEHOG PROTEIN C
VAGE (AUTO-).
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Cyprinoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ekker S.C., Ungar A.R., Porter J.A., Moon R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=EMBRYO;
                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                            Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE MEWLY GENERATED N-TERMINAL FRACKENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDITATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON. NOT DETECTED IN THE NOTICHORD OR DEVELOPING FIN BUTTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. INVOLVED IN DORSO-VENTRAL PATTERNING OF THE BRAIN AND IN EARLY PATTERNING OF THE DEVELOPI
                                                                                                                                                                                                                                                                                                        PF01085; HH_signal; 1.
                                                                                                                                                                                                                                                                                                                       ZDB-GENE-980526-41;
PF01079; Hint; 1.
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416 AA;
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27
201
200
270
270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                         SONICHHOG
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416
200
416
201
270
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                                                                                  46576
               56.4%;
                                                                                                                                                                                                                                                                            Autocatalytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greenstein P., von Kessler Beachy P.A.;
                                                                                WW.
                                                                                                                                                                                                                                                                                                                                           TWHH.
Score 1226.5;
Pred. No. 1.2e
53; Mismatches
                                                                              SIMILARITY).
CHOLESTEROL (BY SIN
61EC2218309CFE59
                                                                                                                                                                                           TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
                                                                                                                               ESSENTIAL
                                                                                                                                                SIMILARITY)
                                                                                                                                                             CLEAVAGE (AUTO-).
INVOLVED IN AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ostariophysi; Danio.
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                                                                                                                               FOR AUTO-CLEAVAGE
                                                                                               (BY SIMILARITY)
                               DB 1;
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                               Length
                                                                                                                                                                                             PROTEIN.
PRODUCT
PROTEIN C-PRODUCT
                                                                                                                                                               (BY
                               416;
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MBL outstation -
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RESULT 13
-I- SUBCLIULAR INCANION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-I- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE NOTOCHORD.
-I- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT THE MID-GASTRULA STAGE.
DISAPPEARS AT THE END OF THE SOMITOGENESIS.
-I- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HES NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (ECHIDNA HEDGEHOG PROTEIN).
INH OR EHH.
                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 382:452-455(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96310864.
Currie P.D., Ingha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97075114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Induction of a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             DIFFERENTIATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGEDWYYYESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLRLFHSLAWGSWT------PGEGVHWYPQLLYRLGRLLLEEGSFHPLGM
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RESULT 14
DHH_MOUSE
ID DHH_MO
AC Q61488
AC Q61488
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT DESERT

DHH_MOUSE STANDARD; Q61488; 15-JUL-1999 (Rel. 38, Cre 15-JUL-1999 (Rel. 38, Las 15-JUL-1999 (Rel. 38, Las DESERT HEDGEHOG PROTEIN P

38, Created)
38, Last sequence update)
38, Last annotation updat
ROTEIN PRECURSOR (DHH) (HH

(DHH) (HHG-3).

update)

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
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QRLAHWAFAPLRLLY----
                                                                                                                                                                                                                                                                                                                                   RLHFCLVLL---LLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASG
                                                                                                                                                                         VHCSVKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAM-GEDGSP--TFSD
                                                                                                                                                                                                                             KLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAH
                                                                                                                                                                                                                                                                   RYEGKVTPSSERFKELTPNYNPDIIFKDEENTGADRMMTQRCKDKLNSLAISVMNLWPGV
                                                                                                                                                                                                                                                                                RYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGV 125
                          HHLAQLAFWPLRLFHSLAWGSWT-PGE----GVHWYPQLLYRLGRLLLEEGSFHPLGM
                                                    AQVGQCLLL---
                                                                          VQPGQYVLVAGVPGLQPARVAAVSTHVAL----GAYAPLTKHGTLVVEDVVASCFAAVAD
                                                                                                        VLTFLDRRPITQKHFYVIRTED-GASVSLTAAHLLFMRVGNCSNRGEPKPGAVRTIFASD
                                                                                                                                 VLIFLDREPHRLRAFQVIETQDPPRRLALTPAHLLF - - - - TADNHTEP - AARFRATFASH
                                                                                                                                                          VHCSVKSEHSVAAKTGGCFPGRALVTMKDGSHRQIRDLQAGDLVLASEGSDGTGDLIYSE
                                                                                                                                                                                                                RLRVTEGWDEDGLHSEESLHYEGRAVDITTSDRDRNKYRMLARLAVEAGFDWVYYESKGH
                                                                                                                                                                                                                                                                                                                     RLSTAAALLTGFILAFSPAYDGCGPGRGYG-KRRTPRKLTPLAYKQFSPNVAEKTLGASG
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PF01079; Hint; 1.
PF01085; HH_signal; 1.
S; PR00632; SONICHHOG.
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                                                                                                                                                                                                                                                                                                                                                                         258;
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                                                 -GKLRKRESQI-THVGVREDQGLYPPLTAHGTVVVNDVLTSCYAAVNR
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                                                                                                                                                                                                                                                                                                                                                                                   55.0%;
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SWTGPDQVLKNGLHWYSQVLIGLGKLLLDSELFHPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         Œ,
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                                                                                                                                                                                                                                                                                                                                                                       Score 1196; D
Pred. No. 4.4e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHOLESTEROL (BY SIMILARITY).
R -> K (IN REF. 2).
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BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                          SITE
                                                                                                                 CHAIN
CHAIN
SITE
                                                                                                                                                                          Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 120-168 FROM N.A. MEDLINE; 95236997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 75:1417-1430(1993).
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                                                                                                     SITE
                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                           EMBL; X76292; CAA53924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 120:3339-3353(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Products, genetic linkage hedgehog gene.";
                                           ACT_SITE
                                                                                                                                                                                                      Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sonic hedgehog, a member of a family of putative nolecules, is implicated in the regulation of CNS
                                                                                                                                                                                                                                                                                                                                                                                                                     AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOT TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INTERCELLULÂR SIĞNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. MAX FUNCTION AS A SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTE DEVELOPMENT.

SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTES. NOT EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIMB BUDS.
PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
                                                                                                                                                                                                                                               MGI:94891; DHH.
; PF01079; Hint; 1.
                                                                                                                                                                                                                    PF01085; HH_signal; 1.
S; PR00632; SONICHHOG.
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198
396
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198
244
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  AA;
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198
396
199
244
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  43542
                                                                                                                                                                                                     Autocatalytic cleavage; Hydrolase;
  M.
                             ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
                                                                                                                   CLEAVAGE (AUTO-)
                                                                                                                               DESERT HEDGEHOG
DESERT HEDGEHOG
                                                          SIMILARITY)
                                                                                      SIMILARITY)
                                                                                                    INVOLVED IN CHOLESTEROL TRANSFER
                                                                       INVOLVED IN AUTO-CLEAVAGE
  AFFEB051BE950FD8
                                                                                                                                                           HEDGEHOG
                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen L.,
SIMILARITY)
FD8 CRC64;
                                                                                                                               PROTEIN C-PRODUCT
                                                                                                                                                           PROTEIN.
                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                           and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signaling; polarity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mohler J.
                                                                                                                                                                                                                                                                                                                                    γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Mus.
                                                                       (BY
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                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                                                                                                                                                                                      Protease;
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                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                    (BY
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Query Match

54.0%;

Score 1175;

DB

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Length 396;

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RESULT 15
DHH_HUMAN
ID DHH_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHH_HUMAN STANDARD; PRT; JYO AA O4323; Q15794; STANDARD; PRT; JYO AA O4323; Q15794; STANDARD; PRT; JYO AA O4323; Q15794 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat DESERT HEDGEHOG PROTEIN PRECURSOR (DHH) (HH
                                                                                                                                                                                                                                                                                                                                                                    "Human desert hedgehog.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY
PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A
SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drummond I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'ISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE OF 85-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM
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                                         SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO "PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-BANGE SIGNALING, WHEREAS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PARLRPRIHECLVLLLLLVVPAAWGCGPGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTL
C-PRODUCT H. SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASLLPLC -- CLALLAL ---- SAQSCGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APLRLLHAL--GALLPGGAVQPTGMHWYSRLLYRLAEELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPLRLFHSLAWGSWTPG-----EGVHWYPQLLYRLGRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYVLVAGVPGLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLLFLDRDLQRRASFVAVETERPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRNHIHVSVKADNSLAVRAGGCFPGNATVRLRSGERKGLRELHRGDWVLAADAAGRVVPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVLAPGGDALQPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endo Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  Y: BELONGS TO THE HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsuya T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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                         (BY SIMILARITY)
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FOR TESTES
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Query Match
Best Local Similarity
Matches 233; Conserv
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SIGNAL
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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367
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                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LVLLLLLVVPAAWGCGPGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIA 72
                                                                                                                                    EHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPH 252
GALLPGGAVQPTGMHWYSRLLYRLAEELL 395
                               GSWTPG-----EGVHWYPQLLYRLGRLLL 396
                                                                                  QPARVAAVSTHVALGAYAPLIKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAW 372
                                                                                                                                                                                                          WDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHVHVSVKA 188
                                                                  RPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL--
                                                                                                                                                                                                                                                                                                                                                     RGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEG
                                                                                                                                                                                                                                                                                                                                                                                                                           LCCLALLALPAQ-SCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
177
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
177
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198
396
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244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 1171.5; DB 1; Length
%; Pred. No. 4.8e-91;
47; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
CHOLESTEROL (BY SIMILARITY).
E -> G (IN REF. 2).
; FCE4FB21972C3AD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESERT HEDGEHOG PROTEIN. PRODUCT.
DESERT HEDGEHOG PROTEIN N-PRODUCT.
DESERT HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (BY
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Search completed: June 5, Job time: 158 sec

2000, 08:19:54

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Run
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                                                                                                                                                                                      419.8
407
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
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          June 5, 2000, 07:56:48; Search time 52.13 Seconds (without alignments) 2969.733 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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        DB
  US-08-176-427B-3
US-08-256-060A-2
US-08-256-060A-4
PCT-US95-02315-1
US-08-356-060A-6
US-08-356-060A-6
US-08-356-060A-7
US-08-356-060A-7
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US-08-356-060A-7
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Sequence 10, X Sequence 1, A Sequence 1, A Sequence 3, A Sequence 5, A Sequence 5, A Sequence 2, A Sequence 1, A Sequence 3, A S
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Query Match
Best Local Similarity
Matches 1051; Conserva
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CITY: Boston
STATE: MA
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ZIP: 02109
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Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Ψ	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 30, Appl	Sequence 30, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli	•	•	Sequence 3, Appli

ALIGNMENTS

ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: HMITELECOMMUNICATION INFORMATION: TELECHONE: (617) 227-7400 TELECAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: Sequence 3, Application US/08176427B Patent No. 5789543 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/176,427 FILING DATE: 30-DEC-1993 CLASSIFICATION: 435 GENERAL INFORMATION: APPLICANT: Ingham, Phillip W. APPLICANT: Memahon, Andrew P. APPLICANT: Tabin, Clifford J. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: LENGTH: 1190 base portion of the TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear E: LAHIVE & COCKFIELD 60 State Street 1190 base pairs Floppy disk US/08/176,427B **HMI-006**

81.2%; 88.3%;

Score 967.6; DB Pred. No. 5e-194; 0; Mismatches 13

DB 2;

Length

1190; 0;

Gaps

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GCCTCCTGCTACGCGGTTCTAGAGAGTCACCAGTGGGCCCACCGCGCCTTCGCCCCTTTG
                                                                                                                               CTGGCGCCCGGCGGGATGCGCTTCGGCCAGCGCGCGTGGCCCCGTGTGGCGCGCGGGAGGAA 960
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION LDATA:
APPLICATION NUMBER: US/08/356,060/
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION NOMBER: US 08/176,427
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7940
TELEFAX: (617) 227-7941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
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GENERAL INFORMATT
                                                                                                                                                                               Matches 1051;
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Em
TITLE OF INVENTION: Proteins and
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
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ADDRESSEE: LAHIVE & COCKFIELD
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CITY: Boston
STATE: MA
COUNTRY: USA
121 GTGCCGCTACTCTACAAGCAATTTGTGCCCGGGCGTGCCAGAGCGGACCCTGGGCGCCAGT
                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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                                                                                                                                                                             Score 967.6; DB 3;
Pred. No. 5e-194;
0; Mismatches 139;
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CTCTTCCTGGACCGGGACTTGCAGCGCCCGGGCTTCATTTGTGGCTGTGGAGACCGAGTGG
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                                CIGGCGCCCGGCGGGATGCGCTTCGGCCAGCGCGCGTGGCCCCGTGTGGCGCGGGAGGAA 950
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                                                 AGACTGCTGCACGCGCTAGGGGCCCCTGCTCCCGGCGGGCCGTCCAGCCGACTGGCATG 1140
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RESULT 3 US-08-176-427B-7

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US-08-176-427B-7
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APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD

STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTOCHMENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-740
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application Patent No. 5789543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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     341
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GAGCCGACCGCTGATGACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTTGGCCATTGCCG
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                                                                  GAGCAGACCGGCTGATGACTCAGAGGTGCAAAGACAAGTTAAATGCCTTGGCCATCTCTG
                                                                                                                               TTAAGGAACTCACCCCCAATTACAACCCCGACATCATATTTAAGGATGAGGAAAACACGG
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RESULT 4
US-08-356-060A-4
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Patent No. 5844079
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                               STREET: 60 St
CITY: Boston
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US-08-356-060A-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sin
Matches 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT IMPORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                  281 GAGCCGACCGCTGATGACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCG
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                                                                                                             TCCGGGCGGCCGCTTTTCCGGGAAATGCAACTGTGCGCCTGTGGAGCGGCGAGCGGA
                                                            TCTACTACGAGTCCCGCAACCACGTCCACGTGTCGAAAGCTGATAACTCACTGGCGG
                                                                                                                                                                                        GCTATGCGCGCAAGCAGCTCGTGCCGCTACTCTACAAGCAATTTGTGCCCGGGCGTGCCAG 160
                                                                                                                                                                                                                                                                                                       TGATGAACATGTGGCCCGGAGTGCGCCTACGAGTGACTGAGGGCTGGGACGAGGACGGCC
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                                     TCTACTATGAATCCAAAGCTCACATCCACTGTTCTGTGAAAGCAGAAACTCCGTGGCGG
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Pred. No. 1e-79;
0; Mismatches 362;
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RESULT 5
PCT-US95-02315-1
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APPLICANT: Ediund,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                    ATTORNEY/AGENT INFORMATION:
NAME: John, P. White
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45375-A-PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1103
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1061
                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                 APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                               COUNTRY:
           TELEPHONE:
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                                                                                                                                                                                       USA
10036
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Edlund, Thomas
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(212) 238-0400
(212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                 Jane
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                                                                                                                                                                                                                                                                                                                                                                           Thomas M.
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           1135
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          TCGTGGCGCCGCACAACGACTCCGGGCCCACTCCGGGACCGAGCCCACTCTTCGCCAGCC 1194
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Best Local Similarity Matches 693; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AC-----CCCAAAAAGCTGACCCCTTTAGCCTACAAGCAGTTTATCCCCAACGTAGCCG
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TTGCCGCTC-----GAGGGCCGGCCGCCCCGCGCAGTTTGCACCGGTGT
                                                                      ACGTGATCGAGACGCGGGAGCCGCGGGAGCGTCTGCTCACTGCCGCGCACCTGCTCT
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nilarity 63.8%;
Conservative
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Pred. No. 4.8e-77;
0; Mismatches 370
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                                               ; NAME/KEY:
; LOCATION:
US-08-356-060A-6
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US-08-356-060A-6
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                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VIncent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-75941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application Patent No. 5844079
GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1103
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                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                  FEATURE:
                                                                                              MOLECULE TYPE:
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                                                                                                         TOPOLOGY:
                                                                                                                   STRANDEDNESS: single
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CGCGCCGCTCACCGCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGC
                                               CCGGCTCCTGCCCCCCCTGTGCACACCGTGACCCTAAGCGAGGAGGCCGCGGGGCGCCTA 1034
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08748591 Patent No. 5759811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VA
CURRENT APPLICATION NUMBER: US/08/748,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bonifas, Jeanette TITLE OF INVENTION: Mutant Human NUMBER OF SEQUENCES: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2200 Sand
CITY: Menlo Park
STATE: CA
COUNTRY: USA
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                   GATCTCCAGAAACTCCGAGCGATTTAAGGAACTCACCCCCAATTACAACCCCGACATCAT
                                                     GGTGGCAAGGGGCTCCGAGCGCTTCCGGGACCTCGTGCCCAACTACAACCCCGACATCAT
                                                                                   GCAGTTTATCCCCAATGTGGCCGAGAAGACCCCTAGGCGCCAGCGGAAGGTATGAAGGGAA
                                                                                                      GCAATTTGTGCCCGGCGTGCCAGAGCGGAGCCCTGGGCCCAGTGGGCCCAGCGGAGGGGAG
                                                                                                                                                     CAGGGGGTTCGGGAAGAGGAGGCAC-----CCCAAAAAGCTGACCCCTTTAGCCTACAA
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Pred. No. 2.7e-73;
0; Mismatches 370;
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Epstein, Er
Hu, Zhilan
Bonifas, Je
   Jeanette
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SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 822-5070
TELEPAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Local Similarity 61.8%;
les 710; Conservative
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STATE: CA
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STREET: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                        TTTGGACATCACTACGTCTGACCGCGACCGCAACAAGTATGGGTTGCTGGCGCGCCTCGC
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.7e-73;
0; Mismatches 370; Indels
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                                                                                                                                                                                                                                    APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Induc
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-DEC-19
                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IAM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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CITY: Boston
STATE: MA
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  30-DEC-1993
                                                                                                                                                                                                                                                                                                                                           Vertebrate Embryonic Pattern-Inducing
                  US/08/176,427B
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Best Local Similarity
Matches 692; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107074400
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                                                                                                                                                       649 CGGGAACTGCACCGCGGAGACTGGGTTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCCC
                                                                                                                                                                                                                         589 GGCGGCTGTTTCCGGGAAATGCAACTGTGCGCCTGTGGAGCGGGAGCGGAGCGGAAAGGGCTG
                                                                                                                                                                                                                                                                        535 GAGTCCAAGGCGCACATCCACTGCTCCGTCAAAGCAGAAAACTCAGTGGCAGCGAAATCA
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TOPOLOGY: 11r
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                                                                                                  ACGCCGGTGCTGCTTCCTTGGACCGGGGACTTGCAGCGCCCGGGCTTCATTTGTGGCTGTG
                                                                                                                                    GGAGGCTGCTTCCCTGGCTCAGCCACAGTGCACCTGGAGCATGGAGGCACCAAGCTGGTG
                                                                   AGTGACTTCCTCACCTTCCTCGACCGGATGGACAGCTCCCGAAAGCTCTTCTACGTCATC
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227-5941
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08356060A Patent No. 5844079 GENERAL INFORMATION:
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                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vertebrate Embryonic Pattern-Indu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: ASCII(t
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435
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CITY: Boston
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USA
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                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE:

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GCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTCCTGCTACGCCGTCATCGAGGAG 1074
                                                                                                                                                                                                                                                                                                                                                                                                    CGGGAACTGCACCGCGGAGACTGGGTTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCC 708
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                            GCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGT 1047
                                                          GCGTCTGTCCACAGCGTCTCATTGCGGGAGGAGGCGTCCGGAGCCTACGCCCCACTCACC
                                                                                       GCGCGCGTGGCCCGTGTGGC---GCGGGAGGAAGCCGTGGGCGTGTTCGCGCCGCTCACC 987
                                                                                                                                                   -----CGGCTACGCGCTGGGGACTCGGTGCTGGCGCCGGGGGGATGCGCTTCGGCCA 930
                                                                                                                                                                                   CCCCAGCACCAGCCAGTCGGAGGCCCACCAGGGCTCCACCAGTGGCCAGGCGCTCTTCGCCAGC
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                                                                                                                                                                                                                                                                                                         AGTGACTTCCTCACCTTCCTCGACCGGATGGACAGCTCCCGAAAGCTCTTCTACGTCATC 774
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Pred. No. 1e-71;
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US-08-176-427B-5
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Patent No. 5789543
                                                                                                                                                         Query Match
Best Local Similarity
Matches 552; Conservat
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: EMI-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1077400
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APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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ADDRESSEE: LAHIVE &
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                    274 AACAGTGGAGCCGACCGCTGATGACCGAGCGTTGCAAAGGAGAGGGTGAACGCTTTGGCC 333
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CITY: Boston
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    AACACGGGTGCCGACCGCCTCATGACCCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC
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                                                                              GAGCGCTTCAAAGAGCTCACCCCCAACTACAATCCCGACATCATCTTCAAGGACGAGGAG
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                                                                                                                                                       Score 355.8; DB 2; pred. No. 2.2e-66; 0; Mismatches 327;
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
                                                                                                                                                     NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HII-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%;
Best Local Similarity 62.8%;
Matches 552; Conservative
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APPLICATION NUMBER: US 0
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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LOCATION:
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CLASSIFICATION: 435
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TOPOLOGY: li
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GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC
                                        TCATTTGTGGCTGTGGAGACCGAGTGGCCTCCACGCAAACTGTTGCTCACGCCCTGGCAC
                                                                                                            GCCCGGGTGGTGCCCACGCCGGTGCTGCTTCCTTGCACCGGGACTTGCAGCGCCGGGCT 753
                                                                                                                                                                            GAGCGTGTGGCCCTGTCAGCTGTAAAGCCAGGAGACCGGGTGCTGGCCATGGGGGAGGAT
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                                                                                     GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA
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Pred. No. 2.2e-66;
0; Mismatches 327;
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RESULT 12 US-08-356-060A-3

Sequence 3, Application Patent No. 5844079

GENERAL INFORMATION:
APPLICANT: Ingham,

Ingham, Phillip W.

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: U. ZIP: 02109

USA

ADUAL STREET: U. STREET: BOSTON MA

60 State Street

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; NAME/KEY:
; LOCATION:
US-08-356-060A-7
                                                                                                                                                 REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
REFERENCE/DOCKET NUMBER: HMI-006CP
REFERENCE (617) 227-7400
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-7941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 939 base pairs
                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/:
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW 1.6 700
REGISTRATION MATTHEW 2.6 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
                                                             FEATURE:
                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: E
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                                                                                                     TOPOLOGY: 11
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ZIP: 02109
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STATE: MA
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                                                                                                     linear
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Query Match

28.2%;

Score 335.6;

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Length 939;

US-08-176-427B-9

Sequence 9, Application US/08176427B Patent No. 5789543 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

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835 GGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGGCGTCTCCTGCTAG
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Mismatches 334;
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RESULT 13 US-08-356-060A-7

841 CTGGCTCAGTTGGCCTTCTGGCCCCCTGCGACTGTTTCCC 879

TGGGCGCACCGCCTTTGCCCCCTTGAGACTGCTGCAC

1092

GGACACTIGTGGTGGAGGATGTGGTGGCCTCCTGCTTTGCAGCTGTGGCTGACCAT 840 GGGACGCTGCTGCAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGTCACCAG 105: CGGGTGGCAGCTGTCTCCACCCACGTGGCCCTTGGGTCCTATGCTCCTCTCACAAGGCAT

Sequence 7, Application US/08356060A Patent No. 5844079 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.

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AGCCATGTGCAACCAGGCCAATATGTGCTGGTATCAGGGGTACCAGGCCTCCAGCCTGCT

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CGCCGGCTACGCGCTGGGGACTCGGTGCTGGCGCCGGGGGGATGCGCCTTCGGCCAGCG 933 CIGCICTICATIGCGGACAATCATACAGAACCAGCAGCCCACTICCGGGCCACATITGCC 660

CGCGTGGCCCGTGTGGCGCGCGGAGGAAGCCGTGTGGGCGTGTTCGCGCGCCGCCTCACCGCGCAC 993

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CTGGTGTTTGCCGCCTCGAGGGGCCGCCCGCGCCAGGCGACTTTGCACCGGTGTTCGCG

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US-08-176-427B-9
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthey P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REGISTION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HM:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227,7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Proteins and MUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1256 base pairs TYPE: nucleic acid? STRANDEDNESS: both TOPOLOGY: linear
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                                                                                                                                                                 GATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGCAAC 471
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      TCCAAAGCCCACATTCATTGCTCTGTCAAAGCAGAAAATTCGGTTGCTGCGAAATCTGGG 588
                                                                                                                                                                                                                                                                                                                                  CTCATGACACAGAGATGCAAAGACAAGCTGAACTCGCTGGCCATCTCTGTAATGAACCAC 348
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                                            TGGCCAGGGGTTAAGCTGCGTGTGACAGAGGGCTGGGATGAGGACGGTCACCATTTTGAA 408
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Pred. No. 4.1e-58;
0; Mismatches 403;
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US-08-356-060A-5
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5,
                                                         APPLICATION NUMBER: US/08/
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HM.
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LABLE Street
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 02109
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                     HMI-006CP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
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                 892
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STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                       AAGTATGGGTTGCTGGCGCGCCTCGCAGTGGAAGCCGGCTTCGACTGGGTCTACTACGAG
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                                                                                                                                                  GAACTGCACCGCGAGACTGGGTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCCACG 711
                                                                                                                                                                                                                                                                                                                                                                                                                           CTGATGACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCGTGATGAACATG 351
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                                          AACTCAACGGAAGATCTCCACACCATGACCGCCGCGTATGCCAGCAGTGTCAGAGCCGGA 888
                                                                    GGGCCGGCGCCCAGGCGACTTTGCACCGGTGTTCGCGCGCCGGCTACGCGCTGGG
                                                                                               ACGCAAGAACCCGTTGAAAAGATCACCCTCACCGCCGCTCACCTCTTTTTGTCCTCGAC
                                                                                                                       ACCGAGTGGCCTCCACGCAAACTGTTGCTCACGCCCTGGCACCTGGTGTTTGCCGCTCGA
                                                                                                                                                                                                         GACCTGAACCCCGGAGACAAGGTGCTGGCGGCAGACAGCGCGGGAAACCTGGTGTTCAGC
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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ATGGCTCTCCTGACCAATCTACTGCCCTTGTGCTGCTTGGCCACTTCTGGCGCTGCCAGCC

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Query Match
Best Local Similarity
Matches 1190; Conserv

Conservative

Score 1190; DB 1; ; Pred. No. 1.4e-238; 0; Mismatches 0;

Length 1190;

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PT A new method to regulate muscle growth
PS Disclosure; Page 106-108, 130pp; English,
PS Disclosure; Page 106-108, 130pp; English,
PS Disclosure; Page 106-108, 130pp; English,
PS This nuclectide sequence comprises a coding region for the human
CC Desert hedgehog protein Dhh (see V05517). The invention relates to
CC a method for modulating the formation and/or maintenance of muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC termyrogenitor cells, in vitro or in vivo, with a hedgehog
CC constructs) or ptc therapeutic (i.e. a small organic molecule that
CC minics the effect of hedgehog proteins on patched signalling, or
CC constructs) or ptc therapeutic or filesorders of, or surgical or
CC activates or potentiates patched signalling) in an amount effective
CC to alter the growth state of the treated cells. Also claimed is a
CC method for treatment or prevention of disorders of, or surgical or
CC cosmetic repair of, such muscle tissues, by administering a
CC muscle atrophy, in particular skeletal muscle atrophy or cardiac
CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The
CC myoblastic growth of muscle tissue such as in myoblastic or
CC mostle atrophy competitie or ptc therapeutic can inhibit growth of
CC myoblastic growth of muscle tissue such as in myoblastic sarcoma
CC (also claimed). The hedgehog therapeutic preferably comprises at
CC (claim and bioactive extracellular portion of a hedgehog protein (see
CC vossiol-19) encoded by a vertebrate hedgehog gene (see X25098-107),
CC especially a human hedgehog gene.

375 C; 424 G; 215 T;
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29-AUG-1998; JU17922.
29-AUG-1797; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Humpi; 99-243557/20.
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cachexia; muscular myopathy; myoblastic sarcoma; therap
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Sequence 1188 BP; 179 A; 376 C; 419 G; 214 T;
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Best Local Similarity
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14-APR-1998; JP-117873.

25-APR-1997; JP-121578.

(HAYB ) HAYASHIBARA SEIBUTSU K
Ariyasu T, Nakamura S, Orita K
WPI; 98-546042/47.
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Claim 10;
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28-OCT-1998:
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14-APR-1998; JP-117873.

25-APR-1997; JP-111578.

(HAYB) HAYASHIBARA SEIBUTSU K

Ariyasu T, Nakamura S, Orita K

MPI; 98-544642/47.

P-PSDB; W79594.
This cDNA sequence codes for a precursor (see W79594) of a novel This cDNA sequence codes for a precursor (see W79594) of a novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified following screenings of human cell lines by PCR using primers (see V62402-03) based on the mouse Desert hedgehog gene. These screenings
                                                                                                                                                                                                                                        02-FEB-1999 (first entry)
Human Desert hedgehog protein
Desert hedgehog; HuDHH; human;
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Claim 9; Page 22-23;
                                                                               Human Desert hedgehog
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Sequence 1122 BP; 170 A; 351 C; 403 G; 198 T;
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0; Mismatches 6;
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                                                                                               Disclosure; Page 94-95; 130pp; English.

CC This nucleotide sequence comprises a coding region for the mouse CC Desert hedgehog protein Dhh (see Y05511). The invention relates to CC a method for modulating the formation and/or maintenance of muscle CC tissue by ecotopically contacting muscle cells, especially muscle CC tissue by ecotopically contacting muscle cells, especially muscle CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog polypeptides and gene therapy CC constructs or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or CC cosmetic repair of, such muscle tissues; by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The compoblastic growth of muscle tissue to provide treatment of hyperblastic or cc neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (constitute extracellular portion of a hedgehog protein (see CC 905510-19) encoded by a vertebrate hedgehog gene (see X25098-107), CC especially a human hedgehog gene.

371 C; 399 G; 226 T;
                             Query Match
Best Local Similarity
Matches 1052; Conserv
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Bladgen CS, Currie PD, Hughes
WPI; 99-24355//20.
P-PSDB; Y05511.
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28-AUG-1998:--017922.
29-AUG-1997; US-057394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse Desert hedgehog protein Dhh cDNA.

Desert hedgehog; Dhh gene; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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                                          GCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTTGCCCCCTTG
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Claim 5; Page 135-37; 210pp; English.

Claim 5; Page 135-37; 210pp; English.

The sequence encodes a mouse desert hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and has been isolated by tow stringency screening of a mouse genome DNA library, in phage laws and the sequence contains 3 homologous regions, encoding a claim open reading frame interrupted by introns. Splicing has confirmed by polymerase chain reaction amplification of first strand cDNA generated from adult testicle RNA. Probes and primers derived from hedgehog sequences may be used as diagnostic agents.

C and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

So Sequence 1190 BP; 194 A; 371 C; 399 G; 226 T;
                                                                                                                                                                                                                                                               Query Match
Best Local :
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13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
WPI; 95-25060/33.
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Q91642;
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Mouse; desert hedgehog gene; probe; primer;
nervous system disorder; gene therapy; antif
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Mouse Dhh hedgehog cDNA sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuron brain infarction; cerebral infarction; transient ischaemic stroke; cerebral infarct volume; spinal cord; oedema; traum

nal cell; attack;

X16183;

standard;

29-APR-1999

(first entry) CDNA; 1190

660

660 600 600

720

540 540 480

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P-PSD; w94469.

Represent the freetheat and prevention of e.g.

conditions - is used for the treatment and prevention of e.g.

per cerebral infarction, stroke and transient ischaemic attacks

per cerebral infarction, stroke and transient ischaemic attacks

per cerebral infarction, stroke and transient ischaemic attacks

per lischaemic or epoxic conditions by administering a ptc (patched)

CC A method has been developed for limiting the damage to neuronal cells by

cischaemic or epoxic conditions by administering a ptc (patched)

CC neuronal cells can also be limited by administering a gene activation

cc construct which recombines with the genomic hedgehog gene to provide a

cc gene. Administration of the ptc therapeutic agent is used to protect

cc gene. Administration of the ptc therapeutic agent is used to protect

cc cerebral tissues against ischaemic injury; to treat cerebral infarct or

cischaemia, stroke (thrombolic or embolic) and transient ischaemic

cinjury to the brain or spinal cord, oedema caused by trauma, haemorrhage

and encephalomyelitis, or in conjunction with (coronary bypass) surgery.

Treatment (which may be prophylactic) is used where ischaemic/epoxic

conditions may cause cerebral hypoxia, or progressive loss of neurons

due to oxygen depletion, including in patients with hypotension. The

treatment reduces CIV by at least 25, particularly at least 70,8. The

present sequence encodes a hedgehog sequence given in the present

convenience 1100 BB. — 104 A. 371 C. 300 C. 305 M.
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Best Local Similarity
Matches 1051; Conserv
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07-JAN-1999.
06-JUN-1998; U13387.
27-JUN-1997; US-883656.
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WPI; 99-095458/08.
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Pred. No. 1.8e-192;
0; Mismatches 139;
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                                                    (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N
WPI; 99-142578/12.
P-PSDB; W97766.
                                                                                                                                                                                                                                                                                                                 Mouse Desert hedgehog (Dhh) cDNA.

Desert hedgehog; Dhh gene; mouse; dopaminergic; GABA-nergic
ptc therapeutic; patched; signal transduction; Parkinson's
ptc therapeutic; patched; signal transduction;
Huntington's disease; amyotrophic lateral sclerosis;
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04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
Increasing the survival cells - by using a ptc 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pf inhibitor, or an agent derived from hedgehog polypeptides, useful in pf the treatment of Parkinson's disease

Disclosure; Page 85-86; 138pp; English.

CC This nuclectide sequence comprises a coding region for the mouse comprises of neurodegenerative disorders.

CC the finding that hedgehog proteins are useful as protective agents coresulting from the loss of form the substantia nigra.

CC established the loss of tissue from the substantia nigra.

CC exemplary disorders include parkinson's disease, Huntington's constructs for constructs and cerebral constructs (i.e. deep the proteins and treats selectorist and cerebral constructs (i.e. deep the proteins and treats and trans-activation constructs for altering hedgehog polypeptides and trans-activation constructs for altering hedgehog gene regulatory sequences) and constructs for altering hedgehog porteins are regulatory sequences) and constructs in both human and animal subjects. Human Inh and Dhh constructs (i.e. agent, and to enhance the implantation of such neurons in cultures, conditions arising from the use of certain drugs, and in the conditions arising from the use of certain drugs, and in the condition and/or treatment of hypoxia, e.g. as a neuroprotective condition and/or treatment of hypoxia, e.g. as a neuroprotective conditions.
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Best Local Sim
Matches 1051;
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                                 CACATCCACGTATCGGTCAAAGCTGATAACTCACTGGCGGTCCGAGCCGGAGGCTGCTTT
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Pred. No. 1.8e-192;
0; Mismatches 139;
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                                             CGGCTGCTGCACGCGCTCGGGGCTCTGCTCCCTGGGGGTGCAGTCCAGCCGACTGCATG
                                                          AGACTGCTGCACGCGCTAGGGGCGCGCTGCCTCCCCCGGGGGCCGTCCAGCCGACTGGCATG
                                                                                          GCCTCCTGCTACGCGGTTCTAGAGAGTCACCAGTGGGCCCACCGCGCCCTTCGCCCCTTTG
                                                                                                       GCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTTGCCCCCCTTG
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                                                                                                                                                                                   CTGGCTCCCGGCGGGACGCGCTCCAGCCGGCGCGCGTAGCCCGCGTGGCGCGCGAGGAA
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EP-874048-A2.
28-OCT-1998.
24-APR-1998; 3
14-APR-1998; J
25-APR-1997; J
antibody

Example 1-2; Page 27-28; 39pp; English.

This cDNA sequence codes for the N-terminal region (see W79597) of a precursor form (see W79595) of novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified in human following ARH-77 (ATCC CRL-1621) cell line following RT-PCR amplification screenings. Further PCR (see V62405-06) yielded cDNA encoding the N-terminal region. DNA molecules (see V62393-95) encoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal
                                                                                                                                                     (HAYB) HAYASHIBARA SEIBUTSU
Ariyasu, Nakamura S, Orita
WPI; 98-544642/47.
P-PSDB; W79597.
                                                                                                                                                                                                                                                                                                                                                       Human Desert hedg
Desert hedgehog;
                                                                                                                                                                                                                                                                                                                                                                                                V62397
V62397;
                                                                                                                                       Human Desert hedgehog
                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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JP-117873.
JP-121578.
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                                                                                                                                                                                                                                                                                                                                                                     hedgehog
                                                                                                                                                                                                                                                                          7. .72
/*tag= a
73. .600
/*tag= b
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Best Local S
Matches 590
 28-OCT-1998.
24-APR-1998; 303187.
24-APR-1998; JP-117873.
14-APR-1997; JP-121578.
25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Ariyasu T, Nakamura S, Orita K;
WPI; 98-544642/47.
P-PSDB; W79598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, DNA and MAb can be used to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses.

Sequence 602 BP; 111 A; 187 C; 199 G; 105 T;
                                                                                                                              Human Desert hedo
Desert hedgehog;
                                                                                                                                                           V62398 standard; cDNA; 575
V62398;
                                                                                                   mat_peptide
                                                                                                                    Homo sapiens.
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                                                                                                                              (first entry)
: hedgehog protein (
shog; HuDHH; human;
                                                                                                  Location/Qualifiers 2. .574
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99.0%;
                                                                                                                                        protein C-terminal
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No. 1.7e-113;
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This cDNA sequence codes for the C-terminal region (see W79598) of a precursor form (see W79594) of novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was coriginally identified in human following RH-7C RTC CRL-1621) cell coriginally identified in human following RF-PCR amplification screenings. Further PCR (see V62407-08) yielded cDNA encoding the C-terminal region. DNA molecules (see V62393-95) encoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, DNA and MAb can be used to elucidate headehog protein, DNA and MAb can be used to elucidate treatments and diagnoses.

So Sequence 575 BP; 66 A; 183 C; 221 G; 105 T;
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Best Local Similarity
Matches 574; Conser
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                                                                                                                                                                                                                                                              CGTGTTCGCGCCGCTCACCGCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTG
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Pred. No. 8.2
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v62396; standard; cDNA; 548 BP. v62396; O2-FEB-1999 (first entry) Human Desert hedgehog protein cl Desert hedgehog; HuDHH; human; Homo sapiens. Location/Qualif.

CDNA

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CDNA clone pHuDHH/#20 codes for a precursor (see W79596) of novel thuman Desert hedgehog protein (see also W79593). Human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified following extensive screenings of human cell lines by PCR using primers (see V62402-03) based on the mouse Desert hedgehog gene. These screenings indicated that the ARH-77 (ATCC CRL-1621) cell line, which is derived from the plasma cell of a leukaemia patient, expressed a specific gene at an elevated level. Sequencing confirmed it to be a novel human gene showing homology to the mouse Desert hedgehog gene. Nucleotide sequences (see W62393-95) cencoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal antibody (MAb) that method for detecting the protein using the MAB. The hedgehog protein, DNA and MAB can be used to eludate hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Sim
Matches 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Ariyasu T, Nakamura S, Orita K;
WPI; 98-544642/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1998.
24-APR-1998; 303187.
24-APR-1998; JP-117873.
25-APR-1997; JP-121578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     morphological abnormalities in humans to establish their treatments and diagnoses.
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GAGTCCCGCAACCACGTCCACGTGTCGGTCAAAGCTGATAACTCACTGGCGGTCCGGGCG
                                         AACAAGTATGGGTTGCTGGCGCGCCTCGCAGTGGAAGCCGGCTTCGACTACTACTAC
                                                                               CAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGC
                                                                                               CAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGC
                                                                                                                                                     ATGTGGCCCGGAGTGCGCCTACGAGTGACTGAGGGCTGGGACGACGACGACGACGCT
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                                                                                                                                      ATGTGGCCCGGAGTGCCCTACGAGTGACTGAGGGCTGGGACGACGACGCCACCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/*tag= a
19. .546
/*tag= b
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 540; DB 1; Pred. No. 6.8e-104;
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                                                                                                                                                                                                                                                                                                                                                                              This cDNA sequence codes for novel human Desert hedgehog protein mature polypeptide (see W79593). Human Desert hedgehog protein CDNA (HuDHH) was originally identified following extensive screenings of human cell lines by PCR using primers (see V62402-03) based on the mouse Desert hedgehog gene. These screenings indicated that the ARH-77 (ARCC CRL-1621) cell line, which is derived from the plasma cell of a leukaemia patient, expressed a specific gene at an elevated level. Sequencing confirmed it to be a novel human gene showing homology to the mouse Desert hedgehog gene. Nucleotide sequences (see V62394-95) encoding precursor forms (see W79594-95) of human Desert hedgehog are also claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, ban and MAb can be used to elucidate hereditary morphological abnormalities in humans cused to establish their treatments and diagnoses.

Sequence 528 BP; 101 A; 160 C; 181 G; 86 T;
                                                                                                                                                                                                                                                                                                                         Best Local
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24-APR-1998; 303187.
14-APR-1998; JP-117873.
25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU KJ.
ATIYASU T, Nakamura S, Orita K.
WPI; 98-544642/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody Claim 8; Page 20-21; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-1999 (first entry)
Human Desert hedgehog mature protein
Desert hedgehog; HuDHH; human; ds.
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                                                                                                                                                                                                                                                                            67 TGCGGGCCGGGGGGGGGGTTGGCCGGCGCGCTATGCGCGCAAGCAGCTCGTGCCG
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                                                                           CCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACCGAGCGT
                                                                                                                    CTACTCTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGTGGGCCA 186
                                                                                                                                                                                                                                           TGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCGTGATGAACATGTGGCCCGGAGTGCGC
                                                         CCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACCGAACGT
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                                                                                                                                                                                                                                                                                                            al Similarity
523; Conserv
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                                                                                                                                                                                                                                                                                                            Conservative
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1. .528
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les 5;
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BY The stroke and transient ischaemic or epoxic processed infarction, stroke and transient ischaemic attacks

Proceeding infarction, stroke and transient ischaemic attacks

Proceeding infarction, stroke and transient ischaemic attacks

Proceeding infarction, stroke and transient ischaemic or epoxic

Proceeding infarction, including the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched)

CC hetrapeutic agent to reduce cerebral infarct volume (CIY). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect construct which retain the ptc therapeutic of treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic constructs. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. CC conditions may cause cerebral hypoxia, or progressive loss of neurons cue to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The invention
                                                                            Query Match
Best Local :
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X16188;
29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9900117-A2.
07-JAN-1999.
26-JUN-1998; U13387.
27-JUN-1997; US-883656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahanthappa NK;
WPI; 99-095458/08.
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                                                                            Local Similarity
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                                                                                                                                           1622
                                                             Conservative
                                                                                                                                         BP;
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/*tag= a
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63.5%;
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                                                         Score 453.8; DB 1;
Pred. No. 5.4e-86;
0; Mismatches 407;
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                               GGGCCGTCCAGCCGACTGGCATTGGATTGGTACTCTCGGCTCCTCTACCGCTTAGCGGAGG
                                                                                            CGCACCGCGCTTTTGCCCCCCTTGAGACTGCTGCACGCGCTAGGGGGCGCTGCTCCCCGGCG
                                                                                                                                    CACTGGTGGTGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGG
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                                                                                                                                                                                                                                                                                                    hedgehog polypeptides and gene therapy constructs of constructs of constructs of constructs of constructs of altering hedgehog polypeptides and trans-activation occurring hedgehog yene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. A bioactive polypeptide comprising amino acid residues 28-202 of human Ihh is preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can also be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.

Sequence 1622 BP; 277 A; 549 C; 510 G; 286 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increasing the survival of neuronal, dopaminergic and GABA-nergic reells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease

This nucleotide sequence comprises a coding region for the human continuity that hedgehog protein (see W97763). The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra.

Core the general loss of tissue from the substantia nigra.

Core the general claimed), amyotrophic lateral sclerosis and cerebral cischaemia. The invention relates to hedgehog therapeutics (i.e., hedgehog nolvention relates to hedgehog for a constructs.
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Human Indian hedgehog (Ihh) cDNA.
Indian hedgehog; Ihh gene; human; dopaminergic; GABA-nergic
ptc therapeutic; patched; signal transduction; Parkinson's
Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, Pang
WPI; 99-142578/12.
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30; Conservative
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Sequence 1622 Bp; 277 A; 549 C; 510 G; 286 T;
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04 MAR-1999
28-AUG-1998; U17922
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SI
WPI; 99-243557/20.
P-PSDB; Y05516.
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Indian hedgehog; Ihh gene; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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GCCACCACGCTCAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTG
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Sonic hedgehog protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C:Date: 07-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C:Accession: A49425
R:Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMa Cell 75, 1417-1430, 1993
A:Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implic A; Reference number: A49425; MUID:94094334
A; Accession: A49425
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-437 cECH>
A; Roste: authors translation is shown for the codon TCC at position 436
C; Genetics:
A; Gene: Shh
C; Superfamily: sonic hedgehog protein
RESULT 3
B53193
hedgehog homolog vhh-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Apecies: Rottus norvegicus (Norway rat)
C;Apecies: Nordan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: B53193
R;Reelink, H.; Augsburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz i Altaba, A.;
Cell 76, 761-775, 1994
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgeh
A;Reference number: A53193; MUID:94170375
A;Accession: B53193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-437 <ROE>
A;Cross-references: GB:L27340; NID:g452122; PIDN:AAA20999.1; PID:g452123
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Les 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       TWLL 422
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C; Superfamily: sonic hedgehog protein
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patterning protein Sonic hedgehog precursor - chicken C.Species: Gallus gallus (chicken) C.Species: Gallus gallus (chicken) C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999 C;Accession: A49424 R.R.Riddle, R.D.; Johnson, R.L.; Laufer, E.; Tabin, C. Cell 75, 1401-1416, 1993 A.Title: Sonic hedgehog mediates the polarizing activity of the ZPA. A;Reference number: A49424; MUID:94094333 A;Accession: A49424 A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-425 <RID>
A;Residues: 1-425 <RID>
A;Residues: 1-425 <RID>
A;Residues: CELT2000: NIT: CASSES. DILAGES.
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C;Superfamily: sonic hedgehog protein
F;1-26/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                    1 MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
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WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGEDWVYYE 177
                                                                                     GASGPAEGRVARGSERFRDLVPNINPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
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                                                                 GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
                                                                                                                                                MLLLTRILLVGFIC -- ALLVSSGLTCGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTL 59
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57.8%;
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Pred. No. 1.5e-88;
2; Mismatches 87;
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RESULT
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C;Species: Brachydanio rerio (zebra fish)
C;Species: Brachydanio rerio (zebra fish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: A53193
R;Roelink, H.; Augsburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz i Altaba, A.;
Cell 76, 761-775, 1994
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgeh
A;Reference number: A53193; MUID:94170375
A;Accession: A53193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <ROE>
A;Cross-references: GB:L27585; NID:9452159; PID:9452160
C;Superfamily: sonic hedgehog protein
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.3 nes 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                        AHIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDF
                                                                                                                                                                                                                                                                                                                          NHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN 299
                                                                                     PARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLL
                                                                                                                          PLRLLHALGALL --
                                                                                                                                                                            VI-APGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFA 358
                                                                                                                                                                                                                               IMFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                             MRLLTRVLLVSLLTLSLVVSGLACGPGRG-YGRRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MALLTNLLPLCCLAL-LALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLLFLDRDLQRRASEVAVETEWPPRKLLLTPWHLVFAA---RGPAPAPGDFA---PVFARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
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                                                                                                                                                           VMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFA
precursor -
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African clawed frog
                                                                                                                      --PGGAVQPTGMHWYSRLLYRLAEELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1120; DB 2;
Pred. No. 5.9e-82;
6; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 418;
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C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 10-Dec-1999
C:Accession: S56765
R:Stolow, M.A.; Shi, Y.B.
Nucleic Acids:Res. 23, 2555-2562, 1995
A:Title: Xenopus sonic hedgehog as a potential morphogen during embryogenes: A;Reference number: S56765; MUID:95357169
A;Accession: S56765
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-444 <STOO-
A;Cross:references: EMBL:L39213; NID:g790937; PID:g790938
C;Superfamily: sonic hedgehog protein
                                                                                                                                                     R:Krauss, S.; Concordet, J.P.; Ingham, P.W. Cell 75, 1431-1444, 1993
A:Title: A functionally conserved homolog of A;Reference number: A49426; MUID:94094335
A;Accession: A49426
                                                                                                                                                                                                                                          sonic hedgehog gene shh protein - zebra fish R;Alternate names: local cell-cell interaction signaling protein C;Species: Brachydanio rerio (zebra fish) C;Date: 06-Oct-1994 *sequence_revision 18-Nov-1994 *text_change | C;Rccession: A49426
                                                A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone
C;Superfamily: sonic hedgehog protein
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                                                                                                     A;Status: preliminary; not compared A;Molecule type: nucleic acid A;Residues: 1-415 <KRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSFIC-TLVTPPGLACGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGRYEGK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDVKKLFYVIETS -- QRKIRLTAAHLLFVAQTKVNGTRSFKSVFASNIQPGDLIYTADPK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLA--PG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                395
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51.2%;
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Pred. No. 1e-79;
Score
                                                                                                                                       with
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1069;
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                                                                    (NCBIP: 142459)
BB
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Length
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A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, A;Reference number: A49425; MUID:94094334
A;Accession: C49425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
C49425
Indian hedgehog protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: C49425
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A; Residues: 1-336 <ECH>
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Best Local S
Matches 190
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                                                                                                                                                                                                                                                      RVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFPSLAWGSW 300
                              RVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL--GAL 369
                                                                                                                                                                       AAAKTGGCFPAGAQVRLENGERVALSAVKPGDRVLAMGEDGTPTFSDVLIFLDREPNRLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHVHVSVKADNSLAVRAGGCEPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
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                                                                                   AFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPGLQPA 240
                                                                                                                                                                                                              LAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQRRA 251
                                                                                                                                                                                                                                                                                                                                            ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGRDE
                                                                                                                                                                                                                                                                                                                                                                                 ERFRDLVPNYNPDIIFKDEENSGADRIMTERCKERVNALAIAVMNMWPGVRLRVTEGWDE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNWP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRLLTRVLLVSLLTLSLVVSGLACGPGRG-YGRRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
                                                                                                                        SFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLAPGGDALRPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNHWP 118
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 956.5;
Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                           5.le-69;
ches 86;
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ches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:LO5404
A;Note: it is uncertain whether Met-1 or Met-51 is the initiator A;Note: intron positions were determined from partial DNA sequence R;Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
Cell 71, 33-50, 1992
A;Title: Secretion and localized transcription suggest a role in positive compared with conceptual translation A;Reference number: A43480
A;Reference number: A43480
A;Status: preliminary; not compared with conceptual translation a.Molecule trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: hh protein
C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A46400; JN0501; A43480
R;Tabata, T.; Eaton, S.; Kornberg, T.B.
Genes Dev. 6, 2635-2645, 1992
A;Title: The Drosophila hedgehog gene is expressed specifically
A;Reference number: A46400; MUID:94040725
A;Accession: A46400
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C:Superfamily: sonic hedgehog protein
C:Keywords: transmembrane protein
F:62-82/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L02793; NID:g157609; PID:g157610
A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
C;Comment: This protein is required for cell-cell communicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S66384; NID:g435848; PID:g435849
A;Experimental source: Oregon-R
A;Experimental source: Oregon-R
A;Note: sequence extracted from NCBI backbone (NCBIN:138996, NCBIP:138997)
R;Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, Gene 124, 183-189, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
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A; Residues: 1-471 <TAS>
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A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene req
A;Reference number: JN0501; MUID:93185922
A;Accession: JN0501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-471 <TAB>
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                                                                                                                                                                       118
238
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                                                                                                                                                                                                                                                                                                                                       Local Similarity 49.4 nes 203; Conservative
                                                                                                                                                                                                                                                                          LPGGAVQPTGMHWYSRLLYRLAEELL
                                                                                                                                                                RRHIYCSVKSDSSISSHVHGCFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSE
                                         RNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTP
                                                                                                           PGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYES
                                                                                                                                                                                                            ASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNÆLAIAVMNMW 118
                                                                                                                                                                                                                                                      LSRLTSLVALLLIVLPMVFSPAHSCGPGRG-LGRHR--ARNLYPLVLKQTIPNLSEYTNS
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                                                                                   PGIRLLVTESWDEDYHHGQESLHYEGRAVTIATSDRDQSKYGMLARLAVEAGFDWVSYVS
                                                                                                                                                                                                                                                                                                                                                             45.5%;
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                                                                                                                                                                                                                                                                                                                                       Score 951; DB 2; 1
Pred. No. 2.1e-68;
D; Mismatches 122;
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Gaps

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submitted to the EMBL Data Library, June 19
A; Reference number: H01643
A; Accession: G02735
A; Status: preliminary; translated from GB/E
A; Molecule type: mRNA
A; Residues: 1-94 <DRU>
A; Cross-references: EMBL:U59748; NID:g14012: C; GenetLos:
A; Gene: hDHH
                                                                                                                                                                                         A;Cross references: EMBL: 281540; PIDN:CAB04405.1; GSPDB:GN00023; A;Experimental source: clone F46B3 C;Genettcs: A;Gene: CESP:F46B3.5 A;Map position: 5 A;Introns: 45/3; 200/1; 235/3; 436/3; 561/3; 581/3; 696/3; 742/1;
                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F46B3.5 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T22281 R;Ainscough, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  desert hedgehog - human (fragment)
(;Speciles: Homo sapiens (man)
(;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
C;Accession: G02735
R;Drummond, I.A.
                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: Z19541 A; Accession: T22281 A; Status: preliminary; translated fr
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A; Residues: 1-868 <W
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Best Local s
Matches 93
                                                                                                                                                                                       Map position: 5;Introns: 45/3; 200/1;
                                                                                              Query Match
Best Local Similarity
Matches 63; Conserv
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                        662
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                                            197 GGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVP--TPVLLFLDRDLQRRASFV 254
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                    GGCFSSDTLYTTPSG-KKRMDEIDVGDYVLTAN---RVKTHFTPVTLWIHRESEKLEEFL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILEMDRNLEQMQNFVQLHTD-GGAVLTVTPAHLVSVWQ---PESQKLTFVFADRIEEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RALDITTSDRDRNKYGLLARLAVEAGFDWVYYGS 94
                                                                                                                                                                                                                                                                                                              1-868 <WIL>
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                                                                                                Conservative
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                                                                                            s; Score 209; DB
s; Pred. No. 7.5e
37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            November 1996
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7.5e-09;
hes 83;
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                                                                                                Indels
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                                                                                                24;
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A; Residues: 1-1226 <WIL>
A; Cross-references: EMBL: Z68008; PIDN: CAA92000.1; GSPDB: GN00028; CESP: R08B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status, Free: DAA
A; Molecule type: DAA
A; Residues: 1-1021 <WIL>
A; Cross-references: EMBL: 281560; PIDN: CAB04547.1;
A; Cross-references: clone K02E2
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T24045
                                                                                                                                                   submitted to the EMBL Data A; Reference number: Z19716 A; Accession: T23252
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A; Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein R08B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A: Introns: 53/2; 113/1;
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                                                                                                                                                                                                               R;Lloyd, C
                                                                                                                                                                                                                               C; Accession:
                                                                                                                                                                                                                                 hypothetical protein K02E2.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T23252
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  A; Map
                      A;Gene:
                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012 SALVAATGACFSLDTWVTTPTG-KKRMDQIDIGDYVLTADLE-KTYFTPITLWIHREPEK 1069
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position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 NSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 -LLHALGALLPGGAVQPTGMHWYSRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CESP: R08B4.1
                    CESP: K02E2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVETEWPPRKLLLTPWHLVFAARGPAPA-----PGDFAPVFARRLRAGDSVLAPGGDAL
                                                                                                                                                                                                                                                                                                                                                                                                                            FAPLRLLHALGALLPGGAVQPTG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RASFVAVETEWPPRKLLLTPWHLVFAAR-GPA-----PAPGDFAPVFARRLRAGDSVLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVLNLFGILHMNEIELPTGTAVYKELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLE-----SHQWAHRAFAPLR- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITTE-RGSTLQLTPLHFMYRTKCNESSEFLKILPENHEAILASYLEIGDCVILTENTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYKGKYRQQKIETITRSVRTGIYSPLTNNGRIIVNDMLASCYSEIQQNTLQTTFFWAYDK 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGDALRPARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQ-----WAHRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROEKINOTTRGLKTGIYSPLTKNGRIIVNDMLASCYSEVQANVLQTTYFW---VFNRLRQ 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152/3; 204/3; 272/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%;
                                                                                                                                                                                         Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194.5;
Pred. No. 1.6e
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        1210
                                                                                                                                                                                         November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; DB 2;
1.6e-07;
hes 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354/1; 389/3;
                                                                          GSPDB:GN00023; CESP:K02E2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714/3; 839/3;
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Gaps

7;

877/1;

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R:Thomas, K.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19793
A:Accession: T23754
A:Accession: T23754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T05C12.10 - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T23754; T24513
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A; Residues: 1-1207 <WIZ>
A; Cross-references: EMBL: Z66500; PIDN:CAA91313.1; GSPDB:GN00020; CESP:T05C12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Burton, J.

Rubmitted to the EMBL Data Library, October 1995
A;Reference number: Z19901
A;Accession: T24513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1207 <WIL>
A;Cross-references: EMBL:249968; PIDN:CAA90265.1; GSPDB:GN00020; CESP:T05C12.10
A;Experimental source: clone MI10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 31/3; 87/2; 141/3; 180/2; 203/3; 267/1; 776/2; 794/2; 834/2; 1086/3; 1143/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP:T05C12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone T05C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.9
Best Local Similarity 31.9
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
  1119
                                                                                                                                                                                   1001 EMFYHREPKTRTNFVVLYTK-SGRKLSLTGRHLLPVAECSQVEQYTMNPDGIDVAMRESK 1059
                                                                                            1060 YAEKARKGECVLSIDESGEVIAD-EIVRVGRMINVGIYSPMTVEGSLIVDGVLSSCFSHL 1118
                                            348 ESHQWAHR 355
                                                                                                                  290 FARRLRAGDSVLA--PGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVL 347
                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                               942 AVLADIPGAAGAAGGGRSNCFSADSLYTTYTGQKR-MDELQIGDYYLYPSSGNYLKYEKY 1000
                                                                                                                                                                                                                                                                                                                     185 SVKADNSLAVRAGG-----CFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 979 W---AFDRLRNLIVQYFGDLYLDEIELPTGTSLYKEVL 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 WAHRAFAPIR--LIHALGALLPGGAVQPTGMHWYSRLL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 CFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQRRASFVAVET 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 9.3%; Score 193.5; DB 2;
Local Similarity 27.1%; Pred. No. 1.6e-07;
hes 59; Conservative 41; Mismatches 83;
                                                                                                                                                                                                                    LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAARGPA-----PAPGDFA---PV 289
ESHS-AHK 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECLLIHNGDQFRMQKIDSISKTVSTGIYSPLTENGRILVNDVLASCYSEVQQNVLQTTFF 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVLAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQ----- 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-NGKTLQLTAGHFIYATECRYLPSKNSSLLNSTPERYRHLIDTLPDDSETKLASQLKIG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFSRDTWVTTPSG-KKRMDEIEIGDYVLTADLKTALF-SAITLWIHREPETVQEFLEIKT 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWPPRKLLLTPWHLVFAAR------GPAP-----APGDFAPVFARRLRAG 297
                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 186.5; DB 2;
31.9%; Pred. No. 7e-07;
ative 36; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1021
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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hypothetical protein ZK1037.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Coetnorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 37/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: ZK1037.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z81142; PIDN:CAB03509.1; GSPDB:GN00023; CESP:ZK1037.10 A;Experimental source: clone ZK1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-481 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, October 1996 A; Reference number: Z20401 A; Accession: T27665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                               199 CFPGNATVRLWSGERKGLRELHRGDWVLAADASGR-VVPTPVLLFLDRDLQRRASFVAVE 257
                                                                                                         433 EILDIKRVKKTGIYAPMTSQGHLLVNKIHTSCHSEVDHH 471
                                                                                                                                                                                                                                                                                                                                 314 CFPNDAVVNVYEKAVKRMDELEIGDWVEALDENGEDITFLPVKYWLHRDPEQEAEFLEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 29.6 tes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                RVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESH 350
                                                                                                                                                                                                                        LD-NGETFTLTEKHLVYTTECRONSSELKISWESISAGKVNAGDCFYLAQSEALTKYRLV 432
                                                                                                                                                                                                                                                                          TEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAGDSVLAPGGDAL----RPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3
<u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 182; DB 2;
29.6%; Pred. No. 5.2e-07;
ative 31; Mismatches 73;
2000, 08:17:55
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Search completed: June Job time: 1235 sec

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Result
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1273 . 5 . 5 . 1273 . 5 . 1273 . 5 . 1273 . 1273 . 1273 . 1273 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 1274 . 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
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  US-08-900-220-17
2088
1 MALLTNLLPLCCLA
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SHH_CYNPY
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SHH_MOUSE
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DHH_KENLA
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091035 gallus gall
015465 homo sapien
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0290812 mus musculu
020419 brachydanio
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  between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 PRINTS; PR006:
Developmental
 protein;
 Autocatalytic cleavage; Hydrolase; Protease;
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ALIGNMENTS	IHH_RASEL	IHH_PUNTE	IHH_DEVDE	IHH_DANPU	IHH_DANKE	IHH_DANAT	IHH_CARAU	DHH_DANKE	DHH_BRARE	SHH_PUNCO	SHH_AMBCH
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Ή	15-JUL-1999 (Rel. 38, Created)
Ä	(Rel. 38,
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ñ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
റ്	Catarrhini; Hominid
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₹ 5	Tate G., Endo Y., Mitsuya T.;
ži	[2]
Ŧ	SEQUENCE OF 85-178 FROM N.A.
ດ	IDNEY;
õ	Drummond I.A.;
ã	"Human desert hedgehog.";
F	mitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
'n	-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
ດີດີ	PAITERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A
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ñ	-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
റ്	WITH
റ്	CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
ń	TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
ກີ	-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
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i n	A CHOLESTEROL MOLETY TO THE C-TERMINAL OF THE NEWLY GENERALED N-
·	TERMINAL ERAGMENT (N-DEODICT) THIS COVALENT MODIFICATION ADDEARS
í ń	TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
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റ്	G, WHEI
റ്	C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
ត	-!- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
'n	
, c	This Swiss-PROT entry is copyright. It is produced through a collaboration

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                                      "Sonic hedgehog, a member of a molecules, is implicated in the Cell 75:1417-1430(1993).
                                                                                                  MEDLINE; 94094334.
Echelard Y., Epstein D.J.,
McMahon J.A., McMahon A.P.;
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SEQUENCE OF 120-168 FROM N.A
                                                                                                                                                             STRAIN-129/SV;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                    DESERT
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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ilarity 100.0%;
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Sciurognathi; Murida
                                                                                                                                                                                                                                           Chordata;
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                                                                                                      A.P.;
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ESSENTIAL FOR AUTO-CLEAVAGE (1
SIMILARITY).

CHOLESTEROL (BY SIMILARITY).

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FCE4FB21972C3AD5 CRC64;
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DESERT HEDGEHOG PROTEIN C-PRODUCT.
DESERT HEDGEHOG PROTEIN C-PRODUCT.

CLEAVAGE (AUTO-) (BY SIMILARITY).

INVOLVED IN CHOLESTEROL TRANSFER (E SIMILARITY).
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DEVELOPMENT.

SUBSCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM CELL SURFACE. IS ALSO SECRETED IN ADULT TESTES. NOT EXPRESSED IN LIMB BUDS.

11 TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTES. NOT EXPRESSED IN LIMB BUDS.

12 PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF AN CHOLESTEROL MOIETY TO THE C-TERMINAL FRAMEWORD ACTIVITY TO THE CHARLES OF THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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Chang D.T., Lopez
Zhao R., Seldin M.
                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
-PATTERNING EVENTS DURLING DEVELOPMENT. MAY FUNCTION AS A
SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES
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121
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                                                                                                                VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN 180
                                                                        GPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNWWPG 120
VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN
                                                          GPAEGRVTRGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPG
                                                                                                                                                                                           Similarity
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Seldin M.F., Fallon J.F., Beachy P.A.;
s, genetic linkage and limb patterning
                                                                                                                                                                                                                                              198
396
                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Autocatalytic cleavage; Hydrolase; Protease;
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96.5%;
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ESSENTIAL FO
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INVOLVED IN CHOLESTEROL TRANSFER SIMILARITY).
                                                                                                                                                                                          Score 2008;
Pred. No. 1
                                                                                                                                                                                                                                                   CHOLESTEROL (BY SIMILARITY).
AFFEB051BE950FD8 CRC64;
                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                             INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                  DESERT HEDGEHOG
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                            FOR
                                                                                                                                                                                           .1e-162;
                                                                                                                                                                                                        BB
                                                                                                                                                                                                                                                                                                AUTO-CLEAVAGE
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PRODUCT
PROTEIN C-PRODUCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DESERT HEDGEHOG PROTEIN PRECURSOR 1 (DHH-1) (CEPHALIC
                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene family of Xenopus laevis.";

gene family of Xenopus laevis.";

Development 121:2337-2347(1995).

-!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND SOMITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moon R.T., Beachy P.A.;
"Distinct expression and shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHH1_XENLA
Q91610;
     EMBL; U26349; AAA85163.1; -. PFAM; PF01079; Hint; 1. PFAM; PF01085; HH_signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ekker S.
                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                                                            NEURULA EXPRESSION BECOMES RESTRICTED TO ANTERIOR STRUCTURES, ENCOMPASSING BOTH NEURAL PLATE AND ENNODERMAL CELLS.

PYM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES CEMENT GLAND FORMATION IN EMBRYOS.
SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM CELL, WHILE THE TERMINAL PEPTIDE REMAINS ASSOCIATED WITH CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER COR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE
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                                                                   s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .C., McGrew L.L., Lai C.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95401852.
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; Hint; 1.
; HH_signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
ea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                 EARLY GASTRULA.
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Xenopodinae;
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S. INDUCES ECTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the hedgehog
                                                                                                                                 restrictions
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                                                                                                    and
                                                                                                                                                  EMBL
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                                                                                                                                                     a collaboration -
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Developmental protein; Autoc
signal.
SIGNAL 1 22
CHAIN 23 396
CHAIN 23 197
CHAIN 198 396
SITE 197 198
SITE 197 198
                                                                                                                                                                2_XENLA
DHH2_XENLA
Q91611;
15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                     Eukaryota;
Batrachia;
MEDLINE; 95401852.
Ekker S.C., McGrew L.L., Lai C.-,
Moon R.T., Beachy P.A.;
"Distinct expression and shared a
gene family of Xenopus laevis.";
Development 121:2337-2347(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                          Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                              TISSUE-EMBRYO
                                                                       SEQUENCE FROM N.A.
                                                                                           xenopus
                                                                                                                                                         DESERT
                                                                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                   366
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                                                                                                                                                                                                                                                                                 LGALLPGGAVQPTGMHWYSRLLYRLAEELL
                                                                                                                                                                                                                                                                                                                PYKTATFVLIEAEGHPSKLLVTPNHLLFI---QSSSSAGFLPTFAYRVQIGDLVQIYVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILAICC-GLLLVPVRCCGPGRGPVGRRRYMRK-LVPLHYKQFVPNVPEKTLGASGKSEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                EGWDEDGHHAHDSLHYEGRALDITTSDRDRNKYGMLARLAVEAGFDWVYYESKAHIHVSV
                                                                                                                                                      -1999 (Rel. 38, Created)
-1999 (Rel. 38, Last sequence update)
-1999 (Rel. 38, Last annotation updat
HEDGEHOG PROTEIN PRECURSOR 2 (DHH-2)
                                                                                                  laevis (African clawed frog).
ta; Metazoa; Chordata; Craniata; Vertebrata;
ia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%;
                                                                                                                                                                                                                                                                                                     Autocatalytic cleavage;
                                       Lai C.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1273.5; DB 1;
Pred. No. 1.7e-100;
2; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESERT HEDGEHOG PROTEIN 1 N-PI
DESERT HEDGEHOG PROTEIN 1 N-PI
DESERT HEDGEHOG PROTEIN 1 C-PI
CLEAVAGE (AUTO-) (BY SIMILARII
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
ESSENTIAL FOR AUTO-CLEAVAGE (BY
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774A3EC2268A5EE9
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                                                                                                                                                                                                            PRT;
                     activities
                                          Lee
                                                                                                                                                      on update)
(DHH-2) (HEDGEHOG
                                                                                                                                                                                                                                                                                  395
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                                       J.J.,
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                     of.
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PROTEIN 1 N-PRODUCT.

PROTEIN 1 C-PRODUCT.

) (BY SIMILARITY).
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                                          VOΩ
                      members
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                                          Kessler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                    Amphibia;
Xenopodinae;
                     of the hedgehog
                                                                                                                                                        PROTEIN
                                           D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease;
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Best Local S
Matches 244
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U26350; AAA85164.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOZETY TO THE C-TERMINAL OF THE NEMLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS.

SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
                                                                                                                                                                                            TEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHVHVS 185
                                                                                                                                                                                                                                                        RVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRV 125
                                                                                                                                                                                                                                                                                                                         LLPLCCLALLALPAQSCGPGRGPV-GRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEG 65
               GDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLH
                                              DPYKTATFVLIEAEGHPTKLLVTPNHLLFIKSSSSTG---
                                                                                                                             VKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDR 245
                                                                                                                                                                                                                                           KIRRGSERFIKLVPNYNPDIIFKDEENTGADRLMTERCKDRVNALAISVMNMWPGLKLRV 126
                                                                                                                                                                                                                                                                                                        ILAACCCWLLLLPVRCCGPGRGPVGGRRRYMRR-LVPLLYKQFVPNVPEKTLGASGKSEG
                                                                              DLQRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV-LAPG
                                                                                                              VNTDNSLGVRSGGCFPGTAMVMMETGKKKPLSELKLGDTVFTTDETGLLIHSVVLLFLHR
                                                                                                                                                                           TEGWDEDGHHAHDSLHYEGRALDITTSDRDRNKYGMLARLAVEAGFDWVYYESKAHIHVS
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                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                    Score 1255.5;
Pred. No. 5.6e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESERT HEDGEHOG PROTEIN 2.
DESERT HEDGEHOG PROTEIN 2 N-PRODUCT.
DESERT HEDGEHOG PROTEIN 2 C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSENTIAL F
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHOLESTEROL (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBC23AF85F69DD08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                     .6e-99
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                      88;
                                                -FQPTFAYRVQIGDLIQIYVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 5
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15-JUL-1999
15-JUL-1999
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Q62226;
                                                                                                                                                                                                                                         MEDLINE; 96069744.

"Hall T.M.T., Porter J.A., Beachy P.A.
"A potential catalytic site revealed
the amino-terminal signalling domain
Nature 378:212-216(1995).

-i- FUNCTION: BINDS TO THE PATCHED (P
                                                                                                                                                                                                                                                                                                                                                                                   "Floor plate and motor neuron induction by different concentrations the amino-terminal cleavage product of sonic hedgehog autoproteclysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94094334.

Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J McMahon J.A., McMahon A.P.;

"Sonic hedgehog, a member of a family of putative signaling
                               <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95236997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SONIC HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                     Roelink H., Porter J.A., C. Beachy P.A., Jessell T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95254654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang D.T., Lopez A., von Kessler D.P., Ch
Zhao R., Seldin M.F., Fallon J.F., Beachy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMahon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHH OR HHG1
                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                       Cell 81:445-455(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 120:3339-3353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Products, genetic linkage and limb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364
                                                         FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPERSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE MEURAL TUB AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION (BY 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
           SIMILARITY).

SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTQVQSSKVVRVSVDEQTGVYAPMTEHGTLLVDGVLTSCYATVESHTLAHASLAPLRLFQ 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oules, is implicated in the 75:1417-1430(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
(Rel.
(Rel.
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el. 38, Last sequence upd
el. 38, Last annotation u
PROTEIN PRECURSOR (SHH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                      (1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiang C., Tanabe Y., Chang
                                                                                                                                                                                                                                                                      Beachy P.A., Leahy D.J.;
te revealed by the 1.7-A crystal structure.
ling domain of Sonic hedgehog.";
                                                                                                                                                                                                                                                                                                                                       ANGSTROMS) OF
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E REMAINS ASSOCT
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Mus ,
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Best Local (
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DOMAIN
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-!- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.

-!- INDUCTION: BY RETINOID ACID.

-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ACTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENILAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CAUBITY OF THE MAIL TO AND THE CELL SURFACE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; 3D-structure
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X76290; CAA53922.1; -. PDB; 1VHH; 29-JAN-96.
242
                               242
                                                               182
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                                                                                                                                                            122
                                                                                                                                                                                          62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV
                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:98297; SHH.
                                                                                LLPLCCLALLA-----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG
FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
                              FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA - - - - RGPAPAPGDFAPVFARRLRAG
                                                                                                                                                                                                                          PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                        LLARCFLVILASSLLVCPGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASG
                                                              IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF01079; Hint; 1.
PF01085; HH_signal; I
s; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRODUCT HAS NO SIGNALING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                    198
383
437
                                                                                                                                                                                                                                                                                                                          Conservative
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387
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437
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                                                                                                                                                                                                                                                                                                                                                                                                       47773
                                                                                                                                                                                                                                                                                                                                       58.1%;
58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                       Score 1214;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                          CHOLESTEROL (BY SIMILARITY) POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                      D0EB72F08E7860EF CRC64;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                       No. 2e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                       Length 437
                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                       Gaps
298
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                                                              241
                                                                                            241
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Q63673;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence upd

15-JUL-1999 (Rel. 38, Last annotation upd

SONIC HEDGEROG PROTEIN PRECURSOR (SHH).
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homolog of hedgehog expressed cell 76:761-775(1994).
-!- FUNCTION: BINDS TO THE DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roelink H., Augsburger A., Heemskerk J.,
Ruiz I Altaba A., Tanabe Y., Placzek M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SPRAGUE-DAWLEY; TISSUE-EMBRYONIC FLOOR MEDLINE; 94170375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Floor plate and motor neuron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 EELL 395
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                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSTERIOR LIMB BUD MESENCHYME.

AND POSTERIOR LIMB BUD MESENCHYME.

PM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEANAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL OR THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED ITO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOCENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING SIGNAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS I ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR VHH-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHRAFAPLRLLHA-LGALLP-----GGAV-----
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Ver
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     induction by vhh-1, by the notochord.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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Best Local
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                                        SHH_CHICK STANDARD;
091035;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata;
Neognathae; Galliformes; Phasianidae; Ph
                                  SONIC
                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
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Neognathae; [1]
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                                                                                                       TWLL 422
                                                                                                                                                              QRVYVVAERGGDRRLLPAAVHSVTLREEAAGAYAPLTADGTILINRVLASCYAVIEEHSW
                                                                                                                     EELL 395
                                                                                                                                                                                                                                                 DSVLA---PGGD-ALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQW 352
                                                                                                                                                                                                                                                                             RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISYMNQWPGV 121
                                                                                                                                                                                                                                                                                   PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMMPGV 121
                                                                                                                                   AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPAGIHWYSQLLYHIG 418
                                                                                                                                                                                          FLDRDEGAKKVFYVIETREPRERLLLTAAHLLEVAPHNDSGPTPGP---SPLFASRVRPG
                                                                                                                                                                                                       FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAG
                                                                                                                                                                                                                     IHCSVKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT
                                                                                                                                                                                                                                   VHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL 241
                                                                                                                                                                                                                                                                                                        LLARCFLVALASSLLVCPGLACGPGRG-FGKRQHPKK-LTPLAYKQFIPNVAEKTLGASG 61
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PF01079; Hint; 1.
PF01085; HH_signa
                                  HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                     198
383
437
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K
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57.8%;
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                                 , Last sequence of Last annotation (SHI
                                                                                                                                                                                                                                                                                                                                                                       ₩;
                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                   Score 1203; D
Pred. No. 1.7e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           SONIC HEDGEHOG I
                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY.
0DBFC19F0D1662A0
                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (AUTO-).
INVOLVED IN CHOLESTEROL TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                   CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                   ESSENTIAL FOR
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                                  (SHH)
                                                                     425
      h; Vertebrata;
Phasianinae; (
                                                                                                                                                                                                                                                                                                                                                                                     (BY
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                                                                                                                                                                                                                                                                                                                                                                                                 AUTO-CLEAVAGE
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PRODUCT
PROTEIN C-PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                       CRC64
                                                                                                                                                                                                                                                                                                                                                 Length
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       Gallus
             Archosauria;
                                                                                                                                                                                                                                                                                                                                    40;
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                                                                                                                                                                                                                                                                                                                                   Gaps
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Cell SH:445-455(1995).

Cell SH:445-455(1995).

Cell SH:445-455(1995).

THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN Cell SHOW WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION CELL SASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION CELL STATEMENT SHOULD SHOW THE GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER CONSTITUTIVE SIGNAL FOR A CELL SIGNAL FOR A CELL SHOP SHOULD SHOW THE SIGNAL FOR A CELL SHEET OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL FOR DEVELOPMENT: SIGNAL FOR DEVELOP SHOULD SHOW THE POLARISING SIGNAL FOR PATTERNING OF THE CANTERIOR POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS SPECIAL FUNCTION.

CHARLET OF THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SHEEDER. IS ALSO SECRETED IN STREAM ASSOCIATED WITH THE COMMITTER THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SHEEDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94094333.
Riddle R.D., Johnson R.L., La "Sonic hedgehog mediates the Cell 75:1401-1416(1993).
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                                                                                                                                                                                                                                                                                                                    EMBL; L28099; AAA72428.1; -.
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Beachy P.A., Jessell T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95254654
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                                                                                                                                                                                                                              Developmental protein;
                                                                                                                                                                                                                                                        PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the amino-terminal cleavage product of sonic hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Floor plate and motor neuron induction by different concentrations
                                                                                                                                                                                                                                                                        PF01079; Hint; 1. PF01085; HH_signal;
                                                                                                                                                                                                                                                        PR00632;
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                                                                                                                                                                                                                                                        SONICHHOG
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                                                                                                                                                                                                                              Autocatalytic cleavage;
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                         SIMILARITY).
INVOLVED IN
                                                                SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN C-PRODUCT
SONIC HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-) (PROBABLE).
INVOLVED IN CHOLESTEROL TRANSFER
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polarizing activity
INVOLVED IN AUTO-CLEAVAGE SIMILARITY).
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RESULT 8
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Best Local Similarity
Matches 244; Conser
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15-JUL-1999
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                  Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T.,
Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C.
Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.;
"Cloning, expression, and chromosomal location off SHH and IHH: two
human homologues of the Drosophila segment polarity gene hedgehog."
Genomics 28:44-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SONIC HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q15465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-FETAL LUNG;
hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                 SEQUENCE OF 119-167 FROM MEDLINE; 95236997.
                                                                                                                                                                              Submitted (AUG-1997) to
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                                                                         D.T.,
gene.";
                                               T., Lopez A., Seldin M.F.,
                                                                                                                                                                                                                             OF 1-187 FROM N.A.
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                          genetic linkage
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al. 38, Last sequence update)
al. 38, Last annotation update)
PROTEIN PRECURSOR (SHH) (HHG-1).
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                       von Kessler D.P., Chiang C.,
Fallon J.F., Beachy P.A.;
nkage and limb patterning act:
                                                                                                                                                                                                     Sutterer
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                                                                                                                         N.A.
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                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1198; DB 1;
Pred. No. 4.4e-94;
6; Mismatches 91;
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CHOLESTEROL (BY SIMILARITY).
POLY-THR.
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                                                                                                                                                                                                     Ozersky
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                                                                                                                                                                                                        'O
                       activity of a murine
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                                                                         Simandl B.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
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EMBL; L38518; AA
EMBL; AC002484;
MIM; 600725; -.
MIM; 142945; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULIAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-1- TISSUE SPECIFICITY: EXPRESSED IN ADULT TISSUES.

-1- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERRASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEMLY-SECRETARED NOF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE NEMLY-SECRETARED NOF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE NEMLY-SECRETARED NOF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE NEMLY-SECRETARED NOF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE NEMLY-SECRETARED NOF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE NEMLY-SECRETARE THE C-PRODUCT IS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

-1- DISEASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISEASE THE THE CAUSE OF THE AUTOSOMAL DOMINANT DISEASE: DEFECTS IN SHAPE SIMILARITY.

-1- DISEASE: DEFECTS IN SHAPE AFFECTS THE MIDLINE DEVELOPMENT OF THE FOREBRAIN AND MIDFACE. HPE IS ASSOCIATED WITH SEVERAL DISTINCT FACIES AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES, ANOPETHALMIA OR CYCLOPIA IS SUIDENT ALONG WITH A CONGENITAL ABSENCE OF THE MATURE NOSE, THE LESS SEVERE FORM FERTURES FACIAL DISMORDHIA CHARACTERIZED BY OCULAR HYPERTELORISM, DEFECTS OF THE UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR CORPUS CALLOSUM.
                                            Signal;
SIGNAL
CHAIN
CHAIN
CHAIN
SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way as the content of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             PFAM;
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-!- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsui L.-C., Muenke M.;
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                                                                                                                                                                                                                        Developmental
                                                                                                                                                                                                                                                                                                    PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSOCIATION WITH SMOOTHENED (SMÓ), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR. POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCINED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORPUS CALLOSUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                          PF01079; Hint; 1.
PF01085; HH_signal; 1
S; PR00632; SONICHHOG.
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4; AAB67604.1;
                                                                                                                                                                                                                     protein; Autocatalytic cleavage; Hydrolase;
                                                                                                                                                                                                mutation.
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SONIC HEDGEHOG PROTEIN C-PRODUCT.
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|GVKLRYTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWYYYESK 178
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ESSENTIAL FOR AUTO-CLEAVAGE
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    Tsukurov
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Gastler J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C. Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.; "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog." Genomics 28:44-51(1995).
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandi B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; Products, genetic linkage and limb patterning activity of a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 120:3339-3353(1994).
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There are no rest
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AB018076; AB018075; AB010092; L38517; AAA62178.1; BAA33523.1; -. BAA33523.1; JOINED BAA33523.1; JOINED

institutions as long

(See http://www.isb-sib.ch/announce/

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PF01079; Hint; 1. PF01085; HH_signal;

protein; Autocatalytic cleavage; Hydrolase;

275 272 203 248 202 100 246 259 45264 27 411 202 411 203 248 272 275 W. CHOLESTEROL (BY SIMILARITY)
D -> R (IN REF. 2).
IIL -> LIF (IN REF. 2).
F -> V (IN REF. 2). INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN N-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER () ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY) SIMILARITY) SIMILARITY) INVOLVED 7888AC6B8C0B5647 IN AUTO-CLEAVAGE (BY (BY

Score 1161.5; DB 1; Length 411;

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RT and PTH-Telated PTOTEIN.";

RL Science 273:613-622(1996).

CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF

CC PARTERNING EVENYS DURING DEVELOPMENT. BINDS TO THE PARCHED (PTC)

CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO

CC ACCIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN

CC ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH

CC ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH

CC ENDOCHONDRAL OSSIFICATION: HE C-TERMINAL PEPTIDE DIFFUSES FROM THE

CC OF PARATHYROID HORMONE-RELATED PROTEIN (PTHRP).

CC -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE

CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE

CC CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE

CC CILL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE

CC TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND

CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND

CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND

CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND

CC -!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECUXSIS ACTIVITY

CC AND A CHOLESTEROL MODIETY OF THE WENTY GENERALED N-

CC ACRECEPROL MODIETY OF THE FOLL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF

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CC TERMINAL OF THE FOULD THE COURTY OF THE WENTY GENERALED N-

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CC ACRECEPTOR OF THE FOIL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
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            TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SUBFACE. THE N-PRODUCT IS THE PROTEIN ACTIVITY TO THE CELL SUBFACE SIGNALING, WHEREAS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNSLAVRAGGCFFGNATVRLWSGERKGLRELHRGDWVLAADASGRVVFTFVLLFLDRDLQ 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSWTPG-----EGVHWWPQLLYRLGRLLL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALLPGGAVQPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLRAFQFIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGVPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38, Created)
38, Last sequence update)
38, Last annotation updat
ROTEIN PRECURSOR (IHH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lanske B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
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8; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Segre G.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408
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Best Local Similarity

Matches 232; Conser
IHH_MOUSE STANDARD; PRT; 411 AA. P97812; Q61724; P97812; TUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1NDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (HHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PEO1079; Hint; 1.
PEAM; PEO1085; HH_signal; 1.
PRINTS; PRO0632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U58511; AAC60010.1; -. PFAM; PF01079; Hint; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY). SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                                        RLLHALGALLPGGAVQPTGMHWYSRLLYRLAEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARLILLLSGCAL-LLAPAVRCCGPGR-VVGSRRRPPRKLIPLAYKQFSPNVPEKTLGASG 61
                                                                                                                                                                                                                                                                                                                                        VAVGSGGLQPAEVVGVRGRTDVGAYAPLTRHGTLVVDDVVASCFALVREQQLAQMAFWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLDRDLQRRASEVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYEGKIARNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                    -APGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                 FLDKEPRALTAFHVIETRQPPRRLALTPTHLLFVADNASAPAAQFRPTFASHVQPGHFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
408 /
                                                                                                                                                                                                                                             -SLLGGPGVQGDGVHWYSGLLYRLGRMLL
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44829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1160; DB 1;
Pred. No. 6.9e-91;
0; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
CHOLESTEROL (BY SIMILARITY)
BA397AE2A9357A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIAN HEDGEHOG PROTEIN N-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVED IN AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIAN HEDGEHOG
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            (HHG-2)
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Gaps

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Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning activity of a mur hedgehog gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CD-1; TISSUMEDLINE; 97236802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94094334.
Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J.,
McMahon J.A., McMahon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 120:3339-3353(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 124-172 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sonic hedgehog, a member of a family of putative molecules, is implicated in the regulation of CNS Cell 75:1417-1430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valentini R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-translational
                                                                                                                                                                                                                                                                                                                                                     CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FOR TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: IN THE EMBRYO, DETECTED IN THE DEVELOPING GUT, THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL CONVOLUTED AND PROXIMAL STRAIGHT TUBULE.

DEVELOPMENTAL STAGE: DETECTED AT 10 DAYS POST COITUM (DPC) IN DEVELOPMENTAL STAGE: DATS DAYS DAYS POST COITUM (DDC) IN DEVELOPMENTAL STAGE: DATS DAYS DAYS DAYS POST CONTUCREASES WITH DEVELOPING UROGENITAL SINUS. EXPRESSION INCREASES WITH CESTIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN
                                                                                                                                             PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SUFFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF PARATHYROID HORMONE-RELATED PROTEIN (PTHRP).
SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED IN SCRIETIANTE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95236997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272:8466-8473(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brookhiser W.T., Park J., Yang T., Briggs J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          processing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND AUTOPROTEOLYTIC CLEAVAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signaling polarity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORM
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Best Local Similarity
Matches 230; Conser
                                                                                TWHH_BRARE
Q90419;
15-JUL-1999
15-JUL-1999
15-FEB-2000
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CONFLICT
SEQUENCE
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SIGNAL
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                   Cyprinoidea;
                             Brachydanio rerio (2ebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; C
                                                                       TIGGY-WINKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U85610; AAB49692.1; ALT_INIT EMBL; X76291; CAA53923.1; -. MGD; MGI:96533; IHH.
SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                            ARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTE 127
                                                                                                                                                                                                                                 CLFLLLLLVPAARGCGPGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKI 71
                                                                                                                                                                                                -GALLPGGAVQPTGMHWYSRLLYRLAEELL
                                                                                                                                                                                                                      LQPARVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFPSLA
                                                                                                                                                                                                                                                             NRLRAFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPG
                                                                                                                                                                                                                                                                                QRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLAPGGDA
                                                                                                                                                                                                                                                                                                      SEHSAAAKTGGCFPAGAQVRLENGERVALSAVKPGDRVLAMGEDGTPTFSDVLIFLDREP
                                                                                                                                                                                                                                                                                                                          ADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDL
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(Rel.
(Rel.
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                    Cyprinidae; Rasborinae;
                                                                        HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                          STANDARD;
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383
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AND
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                                                                       Last sequence updatast annotation up PROTEIN PRECURSOR
                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autocatalytic cleavage;
AUTOPROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1154; D
Pred. No. 2.3e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIAN HEDGEHOG
INDIAN HEDGEHOG
INDIAN HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHOLESTEROL (BY SIMILARITY). W -> S (IN REF. 2). 08BE7AD8507C0D9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLEAVAGE (AUTO-).
INVOLVED IN CHOLESTEROL TRANSFER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSENTIAL
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                                                                                                                          PRT;
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                                                                                          update)
                                                                                                                                                                                                395
                    Danio
                                                                                                                          416
                                                                                  update)
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                                                                       (HHWT)
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PROTEIN N-PRODUCT
PROTEIN C-PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                              Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      371
                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                      251
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TISSUE=EMBRYO;

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Query Match
Best Local S
Matches 223
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-I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE: IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-I- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON. NOT DETECTED IN THE NOTOCHORD OR DEVELOPING FIN BUD. DIENCEPHALON. NOT DETECTED IN THE NOTOCHORD OR DEVELOPING FIN BUD. PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE PULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
SITE
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"Patterning activities of vertebrate hedgehog proteins in developing eye and brain.";
Curr. Biol. 5:944-955/1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U30710; AAC59741.1;
131
                                                    129
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                     WDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHYHVSVKA 188
WDEDGHHLEESLHYEGRAVDITTSDRDKSKYGMLSRLAVEAGFDWVYYESKAHIHCSVKA
                                                                                             RGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEG 128
                                                                                                                                                                                                        LCFISLLITPCGLACGPGRG-YGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGKYEGKIT
                                                                                                                                                                                                                                                         LCCLALLALP-AQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01085; HH_signal; 1.
S; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                   al Similarity
223; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZDB-GENE-980526-41; TWHH. PF01079; Hint; 1.
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201
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270
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416
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416
201
270
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46576 MW;
                                                                                                                                                                                                                                                                                                                                      56.6%;
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                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                             Score 1154; D
Pred. No. 2.3e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
CHOLESTEROL (BY SIMILARITY).
; 61EC2218309CFE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE (AUTO-).
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
                                                                                                                                                                                                                                                                                                                DB 1;
2.3e-90;
nes 94;
                                                                                                                                                                                                                                                                                                                                                               Length 416;
                                                                                                                                                                                                                                                                                                                Indels
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C-PRODUCT
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SHH_CYNPY
SHH_CYNPY
Q90385;
Q90385;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Dast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takabatake T., Takahashi T.C., Inoue K., Ogawa "Activation of two Cynops genes, fork head and animal cap explants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOCHEM. BIOPHYS. Res. COMMUN. 218:395-401(1996).

-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVEI IN LIME FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
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INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIEROBLAST GROWTH FACTOR (BFGF) AND FORK HEAD.

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT CA CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOTICE OF THE MEMORY GENERATED NOTICE OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY GENERATED NOTICE OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY GENERATED NOTICE OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY OF A PROPERTY OF A PROPERTY OF THE MEMORY OF A PROPERTY OF THE MEMORY OF A PROPERTY TO THE C-TERMINAL OF THE MEMORY OF A PROPERTY OF THE MEMORY OF THE MEMORY OF A PROPERTY OF THE MEMORY O
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SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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                                                                                                                           (See http://www.isb-sib.ch/announce/
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Best Local (
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                                                                                                    SHAPE STANDAKU;
Q92008; 013170; 013171;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat-
CANTO HENGREHOG PROTEIN PRECURSOR (SHH) (VHH)
   MEDLINE;
Roelink F
                                                             Brachydanio rerio (Zebrafish) (Zebra danio)
Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
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SEQUENCE
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PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                       TISSUE-EMBRYO
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Cyprinoidea;
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 Heemskerk J.,
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Pred. No. 1.96
7; Mismatches
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SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
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L27585; U30711; Z35669;

AAA20998.1; AAC59742.1; CAA84738.1;

or send an email to license@isb-sib.ch).

(See http://www.isb-sib

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SIMILARITY).

SINCLARITY ON THE CONTINUE SERVICE OF SHOULARITY OF SHOULARITY OF SHOULAR LOCATION: THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDITATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TO MEDITATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. ALSO FOUND IN THE NOTOCHORD AND IN DEVELOPING FIN BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DISNCEPHALON.

THE CUDENCY OF THE ANTENIOR SASTRULATION. BY 9.5 HRS OF THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF THE EMBRYONIC MIDHAL DURING GASTRULATION. BY 9.5 HRS OF THE EMERCHAIN. EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE FRAIL TO THE HEAD, THE ANTERIOR BOUNDARY OF EXPRESSION BEING POSITIONED IN THE CENTER OF THE ANIMAL POLE ANTERIOR TO THE PRESUMPTIVE MIDHALING DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL MOIETY TO THE C-TERMINAL POLE ANTERIOR TO THE PRESUMPTION OF THE CHEAVAGE OF THE PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE CETTERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zardoya R., Abouheif E., Meyer A.;
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
closely related to the zebrafish.",
Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
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"The hedgehog gene family in Drosophila and verte pevelopment Suppl. 43-51(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moon
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Cell 76:761-775(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 96083328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developing eye and brain.";
Curr. Biol. 5:944-955(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ekker S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND MEDLINE; 96014264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 30-92 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR, WHI
ACTIVATE THE
PTC REPRESSES
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.T., Beachy !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPRESSES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97075114.
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Beachy P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED ()
THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE
SSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Α.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greenstein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTOPROTEOLYTIC CLEAVAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X
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H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porter J.A.,
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Best Local S
Matches 220
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15-JUL-1999 (Rel
15-JUL-1999 (Rel
15-FEB-2000 (Rel
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SIGNAL
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 SEQUENCE FROM N.A. TISSUE-INTESTINE; MEDLINE; 95357169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE
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                                                                                    Batrachia;
                                                                                                                                                                                                                                       SHH_XENLA
                                                                                                   Xenopus laevis (African clawed
Eukaryota; Metazoa; Chordata; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLRLLHALGALL-----PGGAVQPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMFTDRDSTTRRVFYVTETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGOK
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                                                                                                                                                                                                                                                                                                                       PARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLL
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                                                                                                                                                                                                                                                                                                                                                                                          VMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U51351; AAB38575.1; U51370; AAB38593.1;
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9 (Rel. 38, L:
0 (Rel. 39, L:
EHOG PROTEIN 1
                                                                                     Anura;
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                                                                                                                              38, Created)
38, Last sequence update)
39, Last annotation update)
. 39, Last annotation (VHH-1).
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                                                                                  a; Chordata; Craniata; Vertebrata;
Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1120; DB 1; pred. No. 1.7e-87; 66; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SONIC HEDGEHOG PI
SONIC HEDGEHOG PI
SONIC HEDGEHOG PI
CLEAVAGE (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHOLESTEROL (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                        PRT;
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                                                                                                                     frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cleavage;
                                                                                                                                                                                                                                       444
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PROTEIN
PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PRODUCT.
                                                                                  Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
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 EMBL; L39213; AAC42227.1; --
EMBL; U26314; AAA85162.1; --
EMBL; L35248; AAA49981.1; --
PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

SIMILARITY:

-i- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURPACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-i- TISSUE SPECIFICITY: STONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION IS OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND LOW EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

-i- DEVELOPMENTAL STAGE: FIRST DETECTED AT THE NEURULA (STAGES 16-17).

FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40).

HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
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"Restrictions to floor plate induction by hedgehog and winged-helix

"Restrictions to floor plate induction by hedgehog and winged-helix

"Restrictions to floor plate induction by hedgehog and winged-helix

Mol. Cell. Neurosci. 6:106-121(1995).

"INCION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED
IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND

IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND
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"Distinct expression and shared activities gene family of Xenopus laevis";
Development 121:2337-2347(1995).
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                                                                                                                                                                                  entities requires a license agreement (Su or send an email to license@isb-sib.ch).
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INDUCTION: BY THYROID HORMONE.
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SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
SIMILARITY).
ESSENTIAL FOR AUTO-CLEAVAGE (BY
SIMILARITY).
3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-
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N -> S (IN REF. 3).
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TQSLL -> NSNLCW (IN REF. 3).
DRXTWTLKAVKVEKVDLE -> ESQDHDLEGRGKWRRLILR
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RESULT 1D 75267 AC 0.5 AC 0.5 DT 0.0 DT 0

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PRINTS; PR00632; SONICHHOG.

SEQUENCE 406 AA; 45072 MW;

9D0FFA76 CRC32;

SEQUENCE FROM N.A. SEQUENCE FROM N.A. GATES P.B., BROCKES DEV. Dyn. 0:0-0(1998).
EMBL; AF047466; AACO3108.1; -.

J.P.,

FERRETTI P.;

O57567 PRELIMINARY; PRT; 406 AA.
O57567;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HEDGEHOG SEGMENT POLARITY HOMOLOG.
NOtophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	103	103.5	103.5	106.5	114.5	115.5	135	150.5	161.5	161.5	163	179.5	182	186.5	
4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.1	5 5	5 .5	ა ნ						8.7		
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Q9WDA4	Q9WDA5	Q9WDA6	Q9WDA7	Q9WLZ4	Q9WLZ7	Q9WLZ8	092753	092752	009234	011875	Q9X856	092835	092834	Q94410	P71196	Q9Z4X5	Q23193	P91573	045273	Q94130	Q94128	Q94129	045992	Q21535	
dengue	Q9wda5 dengue viru	Q9wda6 dengue viru	dengue		dengue	8 dengue		dengue		Oll875 dengue viru	Q9x856 streptomyce		O92834 dengue viru			Q9z4x5 streptomyce	Q23193 caenorhabdi	P91573 caenorhabdi	045273 caenorhabdi	Q94130 caenorhabdi		Q94129 caenorhabdi	045992 caenorhabdi	Q21535 caenorhabdi	

ALIGNMENTS

	186 VKSEHSAAAKTGGCFPARALATLESGEKIPIADLEPGHRVLCMDEGGRRTYSDFLTFLDR 245	186 VI	당
	186 VKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDR 245	186 VI	Qy
	126 TEGWDEDGHHSDESLHYEGRAVDITTSDRDRNKYGMLARLAAEAGFDWVYYESKAHIHCS 185	126 TI	B
-	126 TEGWDEDGHHAODSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHVHVS 185	126 TI	Qy
1	66 KIARNSERFKELTPNYNPDIIFKDEENTGADRIMTQRCKDRLNSLAISVMNQWPGVKLRV 125	66 XI	용
	66 RVARGSERFRDLVPNYNDDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRV 125	66 RV	Qy
σ	8 LLAVACALLLGGFGALGCGFGRVIGRRPRPPRLIPLSYKQFLPHVPEXTLGASGRYEG 65	8	용
CO.	7 LLPLCCLALLALP-AQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEG 65	7 LI	Qy
т.	Matches 227; Conservative 49; Mismatches 107; Indels 7; Gaps	hes	Matc
	1 54.8%; Score 1144.5; DB 13; Length 406; Similarity 58.2%; Brod No 2 lo-81.	Query Match	Quer

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RESULT
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Best Local Similarity
Matches 218; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUZUKI T., ICHIRO O., KUROKAWA T.;
"Retinoic acid given at late embryonic stage depresses sonic hedgehog
and Hoxd-4 expression in the pharyngeal area and induces skeletal
malformation in flounder (Paralichthys olivaceus) embryos.";
Dev. Growth Differ. 41:143-152(1999).
EMBL; AB029748; BAA82360 1;
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SHH.
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01-NOV-1999 (TremBLrel.
01-NOV-1999 (TremBLrel.
SONIC HEDGEHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9W7Q9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.
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                                                                                            WVSSLLFSSQPQASAQKDGVHWYSKILYQLGTWLL
                                                                                                                                                                                               AERLQPVTVKRIYTQEHEGSFAPVTAQGTVVVDQVLASCYAVIQDHELAHWALAPVRLAH
                                                                                                                                                                                                                                                                                                 STTRRLFYVIETD-SGQKITLTAAHLLFVGHSNSTERAHRGMSAVFASQVRPGQTVFVLD
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Last sequence update)
Last annotation update)
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Best Local Similarity 53.8%;
Matches 225; Conservative
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Submitted (MAX-1997) to the EI
EMBL; AROUSS23; AAB94412.1; -
HSSP; 062226; 1VHH.
PFAM; PF01085; HL_Signal; 1.
PFAM; PF01079; H1nt; 1.
PRINTS; PR00632; SONICHOG.
                                                                                                                                                                                                                                                                                                                                                                                                073803; PRELIMINARY;
073803; O1-AUG-1998 (TIEMBLIEL 07,
01-AUG-1998 (TIEMBLIEL 07,
01-NOV-1999 (TIEMBLIEL 12,
                                                                                                                                                                                                                                                                                                                                                                         FUGU
SEQUENCE FROM N.A.

GELLNER K., BRENNER S.;

Submitted (MAR-1998) to the

EMBL; AF056116; AAC34384.1;
                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes),
Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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057404;
01-JUN-1998 (TrEMBLrel. 06, Creat
01-JUN-1998 (TrEMBLrel. 06, Last
01-NOV-1999 (TrEMBLrel. 12, Last
SONIC HEDGEHOG-RELATED PROTEIN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Caudata; Salamandroidea; Salamandridae; I
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Pred. No. 1.7e-78;
9; Mismatches 91;
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Best Local Sin
Matches 210;
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Best Local S
Matches 192
                                                                                                                                                                    SHIMELD S.M.;

SHIMELD S.M.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; Y13858; CAA74169.1; -.

HSSP; 062226; 1VHH.

PFAM; PF01085; HH_signal; 1.

PFAM; PF01079; Hint; 1.

PRINTS; PR00632; SONICHHOG.

SEQUENCE 415 AA; 46765 MW; C5BAC408 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O17499 PRELIMINARY; PRT; 415 AA. 017499; O1-JAN-1998 (TrEMBLrel. 05, Created) O1-JAN-1998 (TrEMBLrel. 05, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update) AMPHIHH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q62226; 1VHH.
PFAM; PF01085; HH_signal;
PFAM; PF01079; Hint; 1.
SEQUENCE 442 AA; 49286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branch:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMPHIHH.
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Pred. No. 2.4e-69;
50; Mismatches 113;
                                                                        Score 919; DB
Pred. No. 7.4e-
56; Mismatches
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Best Local
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Submitted (APR-1998) to the EMB
EMBL; AFGD9606; AAC15065.1; -.
HSSP; Q62226; IVHH.
PFAM; PF011095; HH_Signal; 1.
PFAM; PF011079; Hint; 1.
PRINTS; PR00632; SONICHHOG.
SEQUENCE 410 AA; 46071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            061676;
061676;
01-AUG-1998
01-AUG-1998
01-NOV-1999
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoldea;
Euechinoldea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEDGEHOG
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                                                                                                                                NSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQR 249
                                                                                                                                                                                                                                                                                                           DDERFSKLSPNNNDDIVFKDEEGTGADRLMTQRCKDKLNTLAISVMNEWPGIKLRVVEAW
                                                                                                                                                                                                                                                                                                                                   GSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGW 129
                                                                                                                                                                                                                                                                                                                                                                                                        LCLIAL----TQACHPGRS--GKTSHRPRNRTPLQYKQKVPNISEDTFGASGPPEGRIDR
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                                                  RASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLAPGGD---
                                                                                                     SAAAKNSGGCFPGFSQAYLKNGRMISMLDIRVGDEVAVVNNNGELDYSDVIMIVHRKLND
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(TremBLrel. 07, Last sequence update)
(TremBLrel. 12, Last annotation update)
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Pred. No. 3.5e-53;
55; Mismatches 141;
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Best Local S
Matches 123
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Q9WV29
Q9WV29;
01-NOV-1999 (Trembirel. 12, Created)
01-NOV-1999 (Trembirel. 12, Last sequence update)
01-NOV-1999 (Trembirel. 12, Last annotation update)
INDIAN HEDGEHOG PROTEIN (FRAGMENT).
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NON_TER
SEQUENCE
                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Capordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
       SEQUENCE
                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
GARGES P.L., MEYER R.A. JR., BROWN C.A., PRICE D.K.;
"Indian hedgehog in rat.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF162914; AAD45372.1; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GARGES P.L., MEYER R.A. JR., "Desert hedgehog in the rat Submitted (MAY-1999) to the EMBL; AF148226; AAD31927.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-NOV-1999 (TIEMBLIE1.
01-NOV-1999 (TIEMBLIE1.
DESERT HEDGEHOG PROTEIN
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129 AA;
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Last annotation updat
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Pred. No. 1.1e-44;
1; Mismatches 3
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24CF1044 CRC32;
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D Q9YGV7

C Q9YGV7;

C Q9YGV7;

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NAY-1999 (TrEMBLrel. 12, Last annotation update)
DT 01-NAY-1999 (TREMBLFEL. 12, Last annotation update)
DE SONIC HEDGEHOG (FRAGMENT).
DE SONIC HEDGEHOG (FRAGMENT).
OS Ambystoma mexicanum (Axcolotl).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amp
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Best Local Similarity 65.5
Matches 116; Conservative
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Q9XS16;
Q9XS16;
01-NOV-1999 (TEMBLrel. 12, C
01-NOV-1999 (TEMBLrel. 12, L
01-NOV-1999 (TEMBLrel. 12, L
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SEQUENCE
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"Development of Stratum Intermedium and its Role as a Someting Structure During Odontogenesis.";
Signaling Structure During Odontogenesis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF144100; AAD33256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovinae; Bos.
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107; Conserv
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139 ‡
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15961 MW;
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Last annotation updat
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Pred. No. 4.4e-41;
2; Mismatches 9;
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Pred. No. 2.1e-41;
5; Mismatches 36;
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Ambystoma
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Best Local S
Matches 104
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Best Local Similarity
Matches 108; Conserv
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TOROK M.A., IZPIZUM-BELMONTE J.C., GA
TOROK M.A., IZPIZUM-BELMONTE J.C., GA
SUDMILTER (OCT-1997) to the EMBL/GenE
EMBL; AF031480; AAD18128.1; -
HSSP; Q62226; IVHH.
NON_TER 150 150
NON_TER 150 150
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eleutherodactylus coqui.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHH1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Differences in vertebrate limb development revealed direct developing frog E. coqui.", Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databas EMBL, AF113403; AAD23436.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 NOV-1999 (TYEMBLEE). 12, Last sequence update) 01 NOV-1999 (TYEMBLEE). 12, Last annotation updat SONIC HEDGEHOG PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HANKEN J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                       AGFDWYYYESKAHIHCSV
                                                                                                                                                                 AGFDWYYYESRNHVHVSV 186
                                                                                                                                                                                                                 ALAISVMNLWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRERSKYGMLARLAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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138
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150 AA;
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nilarity 72.0%;
Conservative 2!
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    PRELIMINARY;
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15751 MW;
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Pred. No. 1.3e
23; Mismatches
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EMBL/GenBank/DDBJ databases
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Pred. No. 4.2e-40;
5; Mismatches 17
    PRT;
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    185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
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.3e-39;
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124 RVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHVH

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  Query Match
Best Local s
Matches 77
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Best Local S
Matches 109
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O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-NOY-1999 (TrEMBLrel. 12, Last annotation updat
HEDGEHOG PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                      042128;

01-JAN-1998 (TrEMBLrel. 05, Created)

01-JAN-1998 (TrEMBLrel. 05, Last seq

01-NOV-1999 (TrEMBLrel. 12, Last ann
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SEQUENCE
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SEQUENCE
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SEQUENCE FROM N.A.
KEYS D.N., LEWIS D.L., SELEGUE J.E.,
GATES J., SCOTT M.P., (
                                                                                                   Submitted (SEP-1997) to the EMBL; AB007129; BAA22368.1; HSSP: Q62226; IVHH.
                                                                                                                                                     SEQUENCE FROM STRAIN-BBRR;
                                                                                                                                                                                                                   Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                  042128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 0:0-0(1999).
EMBL; AF117742; AAD08931.1;
HSSP; Q62226; IVHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Junonia coenia (Peacock butterfly) (Precis coenia).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Papillionoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                                             Oryzias.
                                                                                                                                                                                                       Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae;
                                                                                                                                                                                                                                                          ME-SHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYS D.N., LEWIS D.L., SELEGUE J.E., PEARSON B.J., GOODRICH L.V.,
JOHNSON R.L., GATES J., SCOTT M.P., CARROLL S.B.;
"Recruitment of a hedgehog regulatory circuit in butterfly eyespot
                                                                                                                                           ARAKI K.;
                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                         179
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                                                                                                                                                                                                                                                                                                                                                                                                                      RNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAA 228
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                                                                                                                                                                                                                                                                                                                                                                                                RSYIHCSVKTESSVGTGA-GCFPSGAVVHTENGP-XDIASLKKGNKVLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYES 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGVRLRVIEGWDEENSHLDNSLHYEGRAVDLTTSDRDHSKNGMLARLAVEAGFDWVFYEN
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                  Similarity
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4 119
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     Conservative
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                20.6%;
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64.1%;
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                                                                                                                                                       EMBRYO;
     23;
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 Score 431; DB
Pred. No. 1.2e
23; Mismatches
                                                                                                                             EMBL/GenBank/DDBJ databases
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Pred. No. 2.4e-38;
6; Mismatches 33
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annotation update)
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                                                                  CRC32;
                DB
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13;
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                           Length 119;
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184 VSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLF 242

RVTEGWDEDGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKAHIH

60

61 CSVKAESSVAAKSGGCFPGSSTVILENGTQRPVKDLQPGDRVLAADYDGNPVYTDFIMF 119

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RESULT ID 22441
AC 0441
AC 044
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Best Local
                                                                     SEQUENCE FROM N.A. KOESTER R., STICK R., LOOSL SUBmitted (JUN-1997) to the EMBL; 297019; CAB09695.1; HSSP; 062226; 1VHH. PFAM; PF01085; HH_signal; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999
01-MAY-1999
01-NOV-1999
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                 Oryzias latipes (Medaka fish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Buteleostei; Acanthopterygii; Atherinomorpha;

Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae;
                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SONIC HEDGEHOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 99051425.
AMORES A., FORCE A., YAN Y.-L
HO R., AMEMIYA C., LANGELAND
POSTLETHWAIT J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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01-NOV-1999 (TrEMBLrel.
DESERT HEDGEHOG PROTEIN
                            NON_TER
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EMBL: AR071236; AND11531.1; -.

HSSP: 062226; IVHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 LLARLAVEAGFDWVYYESRNHVHVSVKA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ERCKERVNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYG 160
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mes 69; Conserv
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(TIEMBLIEL 10, Last sequence up
(TIEMBLIEL 12, Last annotation
EHOG PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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     9180
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                                                                                                                                                                            LOOSLI
                                                                                                                                                  the
  MW;
                                                                                                                                                  [ F., WITTBRODT J.;
EMBL/GenBank/DDBJ
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Pred. No. 1.9e-22;
7; Mismatches 12;
  59BE42B8 CRC32;
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Cypriniformes;
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Matches 61
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        ITTSDRDRNKYGLLARLAVE 168
ITTSDRDKSKYGTLSRLAVE
                                                       61;
                                                      Similarity 76.2
61; Conservative
                                                             16.9%;
76.2%;
80
                                                      15;
                                                      Score 352; DB 1:
Pred. No. 1e-20;
5; Mismatches
                                                                    13;
                                                                   Length 80;
                                                      Indels
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Search completed: June 5, 2000, 08:19:31 Job time: 185 sec

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Title:

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
    Score
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seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6_CCMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June 5, 2000, 08:17:15; Search time 45.88 Seconds (without alignments) 124.612 Million cell updates/sec
    BLOSUM62
Gapop 10.0 , Gapext 0.5
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1 MALLINLLPLCCLA
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    BB
US-08-176-427B-4
US-08-356-060A-9
US-08-356-060A-11
PCT-US95-15923-20
PCT-US95-15923-20
PCT-US95-15923-17
US-08-356-060A-13
PCT-US95-15923-17
PCT-US95-15463-19
PCT-US95-15463-19
PCT-US95-15463-17
PCT-US95-15463-17
PCT-US95-15463-17
PCT-US95-15463-18
US-08-356-060A-16
US-08-356-060A-14
US-08-356-060A-35
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Sequence 4, Appli
Sequence 8, Appli
Sequence 11, Appl
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  GPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPG 120
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Result No.

60 60

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YEER NO. 2.5e-214; YEER NO. 2.5e-214; Mismatches 8; Indels 0; Gaps 0; COSCONYODEDRY REFOUND TYPE OF THE FORMATION OF THE F	mbryonic Pattern-Inducing Uses Related Thereto	ALIGNMENTS	8-176-427B-13 8-356-060A-36 8-176-427B-16 8-176-427B-16 8-356-060A-16 8-356-060A-16 8-356-060A-17 8-176-427B-17 8-356-060A-17 8-176-427B-15 8-356-060A-17 8-356-060A-15 8-356-060A-15 8-356-060A-37 8-366-060A-37 8-

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US-08-356-060A-9
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                                                                                                                             APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOTOGY: 11 near
 Query Match
Best Local Similarity
Matches 382; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MIGHAM, Phillip W.
APPLICANT: MIGHAMON, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL 360
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STATE: MA
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   Conservative
                 96.2%;
96.5%;
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Score 2008; DB 2;
Pred. No. 2.5e-214;
6; Mismatches 8;
                               Length 396;
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                                                                  CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/176,
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-1
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08176427B Patent No. 5789543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
 MOLECULE TYPE:
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                         437 amino acids
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protein
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US-08-356-060A-11

; Sequence 11, Application US/08356060A

; Patent No. 5844079

; Patent No. 5844079
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                    SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/C
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Vertebrate Embryonic Factor TITLE OF INVENTION: Proteins and Uses Related NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
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                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PAEGRVARGSERERDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
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                                                                                                                                                                                                                                us/08/356,0602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 437;
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RESULT 5
PCT-US95-15463-20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                              OURIWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1547
FILING DAMES.
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ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
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SIREET:
CA
CA
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson ... STREET: 4225 Executive Square, Suite 1400
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es 249; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHCSVKAENSVAAKSGGCFFGSATVHLEQGGTKLVKDLRFGDRVLAADDQGRLLYSDFLT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
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58.7%; Pred. No. 1.6e-126;
53. Mismatches 82;
                                                                              PCT/US95/15463
   38,347
                                                                                                            Version #1.30
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REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-509
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: anino acids
OTOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15463-20
                                                                                                                                                                                                                       RESULT 0
PCT-US95-15923-20
; Sequence 20, Application PC/TUS9515923
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine,
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
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Best Local Similarity
                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15923
FILING DATE: 04-DEC-1995
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                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 92037
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                          RESULT
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9502315 GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M.
APPLICANT: Dodd, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                      APPLICANT: ROELINK, HENK
APPLICANT: Ediund, Thomas
TITLE OF INVENTION: HEDGEHC
TITLE OF INVENTION: HEDGEHC
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                             CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                      419 TWLL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 AHRAFAPERLAHALLAALAPARTDGGGGGSIPAAQSATEARGAEPTAGIHWYSQLLYHIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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                                                                                            ADDRESSEE: Cooper & STREET: 1185 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                              COUNTRY:
                                                         STATE:
                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 58.5 es 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
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                    10036
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                                                       New York
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58.5%; Pred. No. 3.5e-126;
vative 54; Mismatches 82;
                                                                                                                                                                                           DNA ENCODING A VERTEBRATE HOMOLOG OF HEDGEHOG, VHH-1, EXPRESSED BY THE NOTOCHORD,
                                                                                                                                                                             THEREOF
                                                                                              Dunham of the
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MEDIUM TYPE:

Floppy disk

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REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 45375-A-PCT

TELECONMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEPAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid
                                                                                                                                                                         Sequence 2, Application US/08176427B Patent No. 5789543
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Best Local Similarity
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                GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/02315 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LLARCFLVALASSLLVCPGLACGPGRG-FGKRQHPKK-LTPLAYKQFIPNVAEKTLGASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AHRAFAPLRLLHA-LGALLPG---------GAVQPTGMHWYSRLLYRLA 391
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                                                                                                                                                                                                                                                                                                                                                                                                   AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPAGIHWYSQLLYHIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLDRDEGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSGPTPGP---SPLFASRVRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.6%; Score 1203; DB 4; Length 437; 57.8%; Pred. No. 5.7e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Mismatches 87; Indels
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-427B-2
                                                                                                                                      RESULT 9
US-08-356-060A-8
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Sequence 8, Application US/08356060A
Patent No. 5844079
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Vertebrate E
TITLE OF INVENTION: Vertebrate E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.4%; Score 1198; DB 1; Best Local Similarity 59.4%; Pred. No. 2e-124; Matches 244; Conservative 56; Mismatches 91;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 227-7400
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STREET: 60
CITY: Bost
STATE: MA
                                                                                                                                                                                                                                              351 QWAHRAFAPLRLIHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL 395
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                                                                                                                                                                                                                                                                                                                                                                                                                     238 PVLLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA--RGPAPAPGDFA--PVFARR 293
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REFERENCE/DOCKET NUMBER: HMI-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                     SWAHWAFAPFRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
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    Embryonic Pattern-Inducing
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-060A-8
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RESULT 10
US-08-748-591-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: ASCII (text) CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              118 WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYE 177
                                                                         360
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                                                                                                                                            300 VKPGQRVYVLGEGGQQLLPASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEH 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNM 117
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CLASSIFICATION:
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ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
                                                                                             QWAHRAFAPIRILHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLITRILLYGFIC -- ALLYSSGLTCGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTL 59
                                                                                                                                                                                                                                                 PVLLFLDRDLQRRASEVAVETEWPPRKLLLTPWHLVFAA--RGPAPAPGDFA--PVFARR 293
                                                                                                                                                                                                                                                                                    GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
                                                                         SWAHWAFAPFRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
                                                                                                                                                                             LRAGDS--VLAPGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESH 350
                                                                                                                                                                                                                DFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN 299
                                                                                                                                                                                                                                                                                                                   SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT 237
                                                                                                                                                                                                                                                                                                                                                            WPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYE 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617)
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30-DEC-1993
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227-5941
) ID NO: 8:
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Pred. No. 2e-124;
6; Mismatches 91;
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Sequence 4,

Application US/08748591

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5759811
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Epstain, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish and Richardson
                                                                                                                                                                                                                                                                                                              180 NHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
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                                                                                                                                                            285 DFAP--VFARRLRAGDSVLA----PGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVN 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2200 Sand Hill Road CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                    ALGPRALFASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILIN
                                        RVLASCYAVIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTA 417
                                                                                                                                                                                                                                            LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA------RGPAPAPG
                                                                                                                                                                                                                                                                                                                                                                   GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLLLARCLLLVLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLTNLLPLCCL-ALLALPAQSCGPGRGPVGRRRYARKQLVPLLIKQFVPGVPERTLGA
PGGAVQP----TGMHWYSRLLYRLAEELL 395
                                                                              DVLASCYAVLESHQWAHRAFAPLRLLHALGALL-----
                                                                                                                                                                                                    LTFLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGP-PSGG
                                                                                                                                                                                                                                                                                    AHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.4%; Score 1177; DB 1; 54.4%; Pred. No. 4.8e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/748,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
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Best Local Similarity 54.48
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REFIGENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
285 DFAP--VFARRLRAGDSVLA----PGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVN 337
                                                                                                                                      179 AHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDF 238
                                                                                                                                                               180 NHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                            120 GVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESR 179
                                                                                                240 LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA-------RGPAPAPG
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESK 178
                                                                                                                                                                                                                                                                                                     SGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWP
                                                                                                                                                                                                                                                                                                                                            SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                            LTFLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGP-PSGG
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US-08-30.

US-08-30.

Sequence 13, Applicac...

Sequence 13, Applicac...

Sequence 13, Applicac...

Sequence 13, Applicac...

Patent No. 5844079

Selent Information: Phillip W.

APPLICANT: Ingham, Phillip W.

APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Potteins and Uses Related Thereto NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멇
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                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                        Query Match
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TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
119
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                                120 GVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 DVLASCYAVLESHQWAHRAFAPLRLLHALGALL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 ALGPRALFASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILIN 357
                                                                                                                                                                                                                                               y Match 56.4%; Score 1177; DB 2; Length 47. Local Similarity 54.4%; Pred. No. 5e-122; ndels 245; Conservative 54; Mismatches 93; Indels
                                                                               59
                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Vincent, Matthew REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 14-DEC
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                                                                                                                                                                                                      1 MALLTNLLPLCCL-ALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA 59
                                                                                                                                                               1 MLLLARCLLLVLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
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  GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESK
                                                                                                   SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                                               SGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWP 118
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                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                     Length 475;
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RESULT 13
PCT-US95-15463-19
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                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application PC/TUS9515463 GENERAL INFORMATION:
                                                                                                                                                                  Matches 243;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 20
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                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 01-DECCLASSIFICATION:
60 GASGRYEGKITRNSERFKELIPNYNPDIIFKDEENTGADRLMTCRCKDKLNALAISVMNC 119
                                                                                                                                                                                     Local Similarity
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                                                                                                      MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
                                                                                 MILLTRILLVGFIC -- ALLVSSGLTCGPGRG - IGHRRHPKK - LTPLAYKQFIPNVAEKTL 59
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4225 Execumery Square, Suite 1400
                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                 59.0%;
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                                                                                                                                                                  54; Mismatches
                                                                                                                                                                               Score 1158; DB 4;
Pred. No. 5.4e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07265/080WO1
                                                                                                                                                                  93;
                                                                                                                                                                                                    Length 425;
                                                                                                                                                                  Indels
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; Sequence 19, Application PC/TUS9515923
; GENERAL INFORMATION:
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 243; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Johns Hopkins University School of Medicine, et TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: Pish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                      TOPOLOGY: bo
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APPLICATION NUMBER: PC
FILING DATE: 04-DEC-19
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4225 Executive Square, Suite 1400 CITY: La_Jolla
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                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
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ZIP: 92037
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                     GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
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GASGRYEGKITRNSERFKELIPNYNPDIIFKDEENTGADRLMTCRCKDKLNALAISVMNC 119
                                                                             MILLITRILLYGFIC -- ALLYSSGLTCGPGRG-IGHRRHPKK-LTPLAYKQFIPNYAEKTL
                                                                                                  MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL
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                                                                                                                                                            ; Score 1158; DB 4;
; Pred. No. 5.4e-120;
54; Mismatches 93;
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                                                                                                                                                                                                    Length 425;
                                                                                                                                                              Indels
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PCT-US95-15463-17
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                                                                                                                                                                                   Best Local Similarity Matches 223; Conserv
                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 416 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-TOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.
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STREET: 4225 Executive Square, Suite 1400
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 WDEDGHHAQDSLHYEGWALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHVHVSVKA 188
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                               GA-LLPGGA----VQPTGMHWYSRLLYRLAEELL 395
MTWLFPARESNVNFQEDGIHWYSNMLFHIGSWLL 402
                                                                      SLKSVTVKRIYTEEHEGSFAPVTAHGTIIVDQVLASCYAVIENHKWAHWAFAPVRLCHKL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-NOV-1993) A.P. McMahon, Harvard University, Divinity Ave., Cambridge, MA 02138, USA 2 (bases 1 to 1191) Bchelard, Y., Epstein, D.J., St-Jacques, B., Shen, L., Mohler, McMahon, J.A. and McMahon, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity [75, 77, 1417-1430 (1993)
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/gene="Dhh"
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/gene="Dhh"
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/prote1n_1d="CAA53924.1"
/prote2n_1d="CAA53924.1"
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YKQFVPSMPERTIGASGPAEGRVTRGSERFRDLVPNYNPDIIFKDEENSGADRLMTER
CKERVHALAIAVMMNPGVRLKVTEGWDEDGHHAQDSLHYEGRALDITYSDRDNKYG
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/db_xref="taxon:10090"
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Patent: US 5789543->
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Ingham, P.W., McMahon, A.P. and Tabin, C. Vertebrate embryonic pattern-inducing
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-007-1999) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA On Feb 19, 2000 this sequence version replaced gi:6728920
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Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank databases. Gensh Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank databases. Gensh Sate, Showa University Fujigaoka Hospital, Department of Surgical Pathology; Fujigaoka 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan (B-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,
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J. Biochem. Mol. Biol. Biophys. 4, 27-34 (2000)
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/db_xref="taxon:9606"
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/gene="hedgehog"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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-ortkamp, A., Lee, K., Lanske, B., Segre, G.V., Kronenberg, H.M. and
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                                                      Regulation of rate of cartilage and PTH-related protein Science 273 (5275), 613-622 (19)
Tabin, C.J.
Direct Submission
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                                           ACGCTGGAGAACGGTGCCCGGACGCCACTGTGGGCCACTGCGGCCCGGGCCAGCGGGTGCTG
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YKQFSPRVPEKTIGASGRYEGKLARNSERFKELTPNYRPDIIFKDEENTGADRLMTOR 
CKDRLNSLAISVMNQWFGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYG 
MLARLAVEAGFDWYYIESKAHIHCSVKSEHSAAAKTGGCFPGRALATLENGARTPHMA 
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LVVDDVVASCFALVREQQLAQMAFWPLKLYHSLLGGPGVQGDGVHWYSGLLYRLGRML
LPPDSFHPLGAPRAES' 260 t 2 others
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00 Longwood, Boston, MA 02115, USA
Location/Qualifiers
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Valentini,R.P., Brookhiser,W.T., Park,J., Yang,T., E Dressler,G. and Holzman,L.B.
Post-translational Processing and Renal Expression c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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/product="Indian hedgehog protein"
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PGVKLRVTEGKDEDGHISEESLHJEGRAVDITSDRDANKYGLLARLAVEAGFDWYJ
ESKAHVHCSVKSEHSAAAKTGGCFPAGAQVRLENGERVALSAVKPGDRVLAMGEDGTP
TFSDVLIFILDREPNRLRAFQVIETQDPPRRLALTPAHLLFIANHTEPAAHFRATFAS
HVQPGQYVLVSGVPGLQPARVAAVSTHVALGSYAPLTRHGTLTVVEDVVASCFAAVADH
HLAQLAFMPLRLFPSLANGSWTPSEGVHWYPQMLYRLGRLLLEESTFHPLGMSGAGS"
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Pred. No. 5.3e-63;
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GGGACCGCAGCAAGTACGGCATGCTGGCTCGCCTGGCTGTGGAAGCAGGTTTCGACTGGG
             GCGACCGCAACAAGTATGGGTTGCTGGCGCGCCTCGCAGTGGAAGCCCGGCTTCGACTGGG
                                           ATCATTCAGAGGAGTCTCTACACTATGAGGGTCGAGCAGTGGACATCACCACGTCCGACC
                                                         ACCACGCTCAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACC
                                                                                     TGATGAACATGTGGCCCGGAGTGCGCCTACGAGTGACTGAGGGCTGGGACGACGACGGCC
                                                                                                                                 GAGCAGACCGGCTGATGACTCAGAGGTGCAAAGACAAGTTAAATGCCTTGGCCATCTCTG
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Location/Qualifiers
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Pred. No. 2.3e-61;
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Sequence 4 from patent
AR063083
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Ingham,P.W., McMahon,A.P. and Tabin,C.
Vertebrate embryonic pattern-inducing
                                       Similarity 64.
01; Conservative
                                                                                                                                                                     Patent:
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Location/Qualifiers
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                                    Score 419.8; DB 5;
Pred. No. 2.3e-61;
0; Mismatches 362;
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                                                                AGAGTCACCAGTGGGCGCACCGCGCTTTTTTGCCCCCTTGAGACTGCTGCACGCGCTAGGGG
                                                                                                    TCACGGCGCACGGCACCATTCTCAATCAACCGGGTGCTCGCCTCGTGCTACGCTGTCATCA
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Submitted (03-NOV-1997) A.P. McMahon, Harvard
Divinity Ave., Cambridge, MA 02138, USA
On Nov 8, 1997 this sequence version replaced
Location/Qualifiers
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Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity Cell 75 (7), 1417-1430 (1993)
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Submitted (24-NOV-1993) A.P. McMahon, Harvard
Divinity Ave., Cambridge, MA 02138, USA
revised by [3]
2 (bases 1 to 1314)
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1 (bases 1 to 1314)
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shh gene; sonic hedgehog protein
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                                                                             Conservative
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25. .1311
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/product-"sonic hedgehog"
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/db_xref="SPTREMBL:Q62226"
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CKDKLNALAISVMNQWPCVKLRVTEGRWEDGHHSEESLHYEGRAVDITTSDRDKSKYG
MLARLAVEAGFDWYYYESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVXD
LRPGDRVYYESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVXD
LRPGDRVAAADDGGRLLYSDFITFLDRDEGAKKVFVIETLEFREERGAYAPL
PHNDSGPTPGPSALFASRVRPGQRVYVVAERGGDRRLLPAAVHSVTLAEEAGGYAPL
TAHGTILINRVLASCYAVIEEHSWAHRAFAPFELAHALLAALAPARTDGGGGGSIPAA
QSATEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPLGMAVKSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/63"
/db_xref="taxon:10090"
/dev_stage="embryo, 8.5 dpc"
/clone_lib="Hogan; lambda gt10"
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/protein_id="CAA53922.1"
/db_xref="GI:2597988"
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Ekker, S.C., McGrew, L.L.,
Moon, R.T. and Beachy, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-MAY-1995) Stephen C. Ekker,
Genetics, Johns Hopkins University, 725 N.
Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moon,R.T. and Beachy,P.A.
Distinct expression and shared activities of hedgehog gene family of Xenopus laevis
Development 121 (8), 2337-2347 (1995)
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U26350
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/protein_id="AAA85164.1"
/protein_id="AAA85164.1"
/db_xref="GI:1147830"
/translation="mpavrilliaacccwilllpvrccgpgrgpvggrrrymrrlvpl
_tykQfvDnvpektlgasgksegkirrgserfiklvpnynpDiifkDeenTgaarkmTe
_RCKDKVNALAISVMNMMPGLK.RVTEEWDEDGHHANSLHYEGRALDITTSDRDRNKY
_GMLARLAGFDWYYESKAHIHVSVUTDNSLGVRASGGCFFTAMVMMETGKKFLIS
_ELKLGDTVFTTDETGLIHSVVLLFLBRDPYKTATFVLIEAEGHPTKLIVPNHLTEI
_KSSSTGFQPTFAYRVQIGDLIQIYVNGTQVQSSKVVRVSVDEQTGVVAPMTEHGTLL
_VDGVLTSCYATVESHTLAHASLAPLRLFQGIASMLPDLHTSDGVHWYCHILYVLAKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="related to Xenopus laevis cephalic hedgehog, encoded by GenBank Accession Number U26349; secrete signaling molecule; Method: conceptual translation supplied by author"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene-"hh4"
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/db_xref="taxon:8355"
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Anura; Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 1.2e-60;
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Nolfe St/714 PCTB,
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Rat (vhh-1) mRNA, or
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Rattus norvegicus strain Sprague-Dawley
Rattus norvegicus
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Roelink, H., Augsburger, A., Heemskerk, J., Korzh, V.,
1 Altaba, A., Tanabe, Y., Placzek, M., Edlund, T., Jess
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//Bb_xref="G1:452123"
//Bb_xref="G1:45212
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/strain="sprague-Dawley"
/db_xref="taxon:10116"
315. .377
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Distinct expression and shared activities hedgehog gene family of xenopus laevis Development 121 (8), 2337-2347 (1995)
                                                Submitted (04-MAY-1995) Stephen C. Ekker, Molecular Biology and Genetics, Johns Hopkins University, 725 N. Wolfe St, 714 PCTB, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis cephalic U26349
                                                                                                      Direct Submission
                                                                                                                Ekker, S.C., McGrew, L.L., Moon, R.T. and Beachy, P.A.
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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TTCATTTGTGGCTGTGGAGACCGAGTGGCCTCCACGCAAACTGTTGCTCACGCCCTGGCA 812
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/protein_id="AAA85163.1"
/protein_id="AAA85163.1"
/protein_id="AAA85163.1"
/db_xref="GI:1147828"
/db_xref="GI:1147828"
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KQFVPNVPEKTLGASGKSEGKIIRGSEEFIELVPNYNDIIFKDEEKTGADRLKYGM
KQFVNALAISVLMMWPGVKLRVTEGWDEDGHHAHDSLHYEGRALDITTSDRDRNKYGM
KQRVNALAISVLMMWPGVKLRVTEGWDEDGHHAHDSLHYEGGFPGTAMVAMGTGERKPLSEL
KIGDTVTTDETGGLITSVVLLFLHRNPYKTAFFVLIEAEGHSKKLLVTPNHLLFVG
SSSAGFLPTFAYRVQIGDLVQIYVNGTQVQSSKVVRVSLEEQTGVYAPMTEHGTLLVD
GVLTSCYATVESHTLAHVSLAPLRLFQGIASMLPDLDMSDGVHWYCHILYVLAKYVLM
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translation supplied by author"
/codon_start=1
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                  Homo sapiens sonic
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L38518.1 GI:663156
homologue; sonic hedgehog protein
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c hedgehog
                                                                           protein
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complete cds.
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Local Similarity 61.9%;
hes 711; Conservative
GGTGAACGCTTTGGCCATTGCCGTGATGAACATGTGGCCCGGAGTGCGCCTACGAGTGAC
                                                                                                                              CAGGGGGTTCGGGAAGAGGAGGCAC-----CCCAAAAAGCTGACCCCTTTAGCCTACAA
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                                                        ATTTAAGGATGAAGAAAACACCGGAGCGGACAGGCTGATGACTCAGAGGTGTAAGGACAA
                                                                                           CTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACCGAGCGTTGCAAGGAGAG
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1576)
Marigo, V., Roberts, D.J., Lee, S.M.K., Tsukurov, O., Levi, T., Gastier, J.M., Epstein, D.J., Gilbert, D.J., Martin, G.G., Copeland, N.G., Seidman, C.E., Jenkins, N.A., Seidman, J.G., McMahon, A.P. and Tabin, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning, expression and chromosomal location of SHH and IHH, two human homologues of the Drosophila segment polarity gene Hedgehog Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Translation="MLLARCLLLVLVSSLLVCSGLACGPGRGFGKRRHPKKLTPLAY KQFIPNVAEKTLGASGRYEGKKSRNSERFKELTPNYNPDIIFKDEENTGADRLMTORC KDKLNALAISVMNOWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGM LARLAVEAGFDWYYYDSKAHIHCSVKAENSVAAKSGGCFGSATWHLEQGGTKLVKDL SPGDRVLAADDGRALLYSDELTFLDRDDGAKKVFYVUTETREPRERLLLJTAAHLLFVAP HNDSATGEPEASSGSGPPSGGALGPRALFASRVRPGQRVYVVAERDGDRRLLPAAVHS VTLSEEAAGAYAFLTAOGTILINRVLASCYAVIEHSWAHRAFAPFRLAHALLAALAP ARTDRGGDSGGDRGGGGRVALTAPGAADAPGAADAPGAGATAGIHWYSQLLYQIGTWLLDSE ALHPLGMAVKSS"

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508 c
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/protein id="AAA62179.1"
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/note="homologue
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152. .1540
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/tissue_lib="Clontech"
/note="vector: lambda (
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/db_xref="taxon:9606"
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                GCTAGGGGC 1103
                                                             GGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTTGCCCCCCTTGAGACTGCTGCACGC 1094
                                                                                                                                                                                                        CCAGGCGACTTTGCACCGGTGTTCGCGCGCCGCCTACGCGCTGGGGACTCGGTGCTGGCG 906
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                                               GGTCATCGAGGAGCACAGCTGGGCGCACCGGGCCTTCGCGCCCTTCCGCCTGGCGCACGC 1305
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Search completed: June 5, 2000, 07:33:10 Job time: 9655 sec

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Listing first 45 summaries
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US-08-356-060A-7
                                         US-08-356-060A-7
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GENERAL INFORMATION:
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Result

45	44	43	42	41	40	39	38	37	36	35	34	<u>3</u> 3	32	ω	30	29	28
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US-08-471-046A-26	US-08-471-046A-17	US-08-463-483A-26	US-08-463-483A-17	US-08-471-044-26	US-08-471-044-17	US-08-471-033-26	-471-033-	US-08-469-334-35	US-08-470-566B-35	US-08-471-046A-35	US-08-463-483A-35	US-08-471-044-35	US-08-471-033-35	US-08-469-334-18	US-08-470-566B-18	US-08-471-046A-18	US-08-463-483A-18
Sequence 26, Appl	•	Sequence 26, Appl	•	Sequence 26, Appl	-	-	•	Sequence 35, Appl	-	-	-	`	`	`	Sequence 18, Appl	-	•

Application US/08356060A

ALIGNMENTS

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47 APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J. STREET: 60 St CITY: Boston

FILING DATE: 14-DEC-1944

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/176.
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 27-7400
TELEPAX: (617) 27-740
TELEPAX: (617) 27-7941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994 02109 US 08/176,427 HMI-006CE

MOLECULE TYPE: FEATURE: NAME/KEY: LOCATION: TOPOLOGY: 111 TYPE: nucleic acid linear CDNA single

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Best Local Similarity
Matches 936; Conserv
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                                  GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCCGTCTCCTGCTAGAAGAGGGCCAGC
                                           GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAAAGAGGGCAGC 1250
                                                                    TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT
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TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 939
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RESULT 2
US-08-176-427B-5
; Sequence 5, Application
; Patent No. 5789543

US/08176427B

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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LCCATION: 1..1056
US-08-176-4278-5
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-193
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617) 227-740
INFORMATION FOR SEQ ID NO: 5:
CEPTURE CANACTERISTICS:
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Best Local
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pair
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STREET: 60 St
CITY: Boston
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                          61
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Local Similarity 88.2%;
nes 928; Conservative
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GCCGCAGCCAAGACGGGCGGCTGCTTCCCCTGCCGGAGCCCCAGGTACGCCTGGAGAGTGGG
                                                                    GACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCG
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                                                     GACTGGGTGTATTACGAGTCCAAGGCCCCACGTGCATTGCTCTGTCAAGTCTGAGCATTCG
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Pred. No. 5.
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Sequence 3, Application Science Scient No. 5844079
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/356,060
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                             APPLICANT: Ingham, phillip w.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021 AACCACTGCCTCCTGGAACTGCTGTGCGTGG 1052
                                                                                                                                                      ADDRESSEE: LA STREET: 60 St CITY: BOSTON STATE: MA COUNTRY: USA ZIP: 02109
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    JMBER: US/08/356,060A
14-DEC-1994
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NAME: VINCENT, MATTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
I ENTRE: 1056 5-2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 928; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                  541
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AGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCC
                                                         CTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGGCCACATTTGCC
                                                                                                                GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC
                                                                                                                                                      GCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCAC
                                                                                                                                                                                             GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA
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                                      CTGCTCTTCATTGCGGACAATCATACAGAACCAGCAGCCCACTTCCGGGCCACATTTGCC
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ilarity 88.2%;
Conservative
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Pred. No. 5.5e-1
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RESULT 3 US-08-356-060A-3

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                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DWA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/081764278
Patent No. 5789543
GENERAL INFORMATION:
APPLICANT: Infoham, Phillip W.
APPLICANT: McMahon, Andrew J.
APPLICANT: Tabin, Clifford J.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
CCRRESSONDENCE ADDRESS:
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
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                                                          CACTCACCGCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTCCTGCTACGCCGTCA
                                                                                      CGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG
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Pred. No. 3.9e-93;
0; Mismatches 360;
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US-08-356-060A-1
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                                                                                                Query Match
Best Local Similarity
Matches 763; Conserv
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APPLICANT: Ingham, Balllip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1127
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
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                                                                                                                                                                                                                                        FEATURE:
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LENGTH: 1277 base pairs
   223
                                                  163 GGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCCAATGTGCCCG 222
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                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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CITY: Boston
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                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                   GGAGGCACCCCAAAAAGCTGACCCCGTTAGCCTATAAGCAGTTTATTCCCAATGTGGCAG 166
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                                                                                                Score 459; DB 3; 1
Pred. No. 3.9e-93;
D; Mismatches 360;
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                                                                        ATTGGTACCCCCAGCTGCTCTACCGCCTGGGGCGCTCTCCTGCTAGAAGAGGGCAGCTTCC
                                                                                                                  TGGCCGCCCTCTGCCCAGATGGGGCCATCCCTACTGCCGCCACCACCACCACTGGCATCC
                                                                                                                                                 CATGGGGCAGCTGGACCCCGGGGGAG----
                                                                                                                                                                                   TCGAGGAGCACAGTTGGGCCCATTGGGCCTCCGCATTCCGCTTGGCTCAGGGGCTGC
                                                                                                                                                                                                                  TGGCTGACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTACGGCTGACAATCACACGGAGCCGG------CAGCCCGCTTCCGGGCCACAT 930
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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/176
APPLICATION UMBER: US 08/176
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT INFORMATION:
NAME: VINCENT INFORMATION:
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-740
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
TYPE: DUCLE: 4610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5844079
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA FEATURE:
205
                                    270
                                                                                                           210
                                                                                                                                                                                 150 GTGGGCAGCCGCCGGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGC 209
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 50
CITY: Boston
                                                                                                                                                                                                                                                                                                / Match 28.0%;
Local Similarity 71.0%;
les 631; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 14-DE
                                                                      AGCTCCGAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGAC 329
                                                                                                                                              TTCGGGAAGAGGAGGCACCCCAAA----AAGCTGACCCCTTTAGCCTACAAGCAGTTTATC 144
                                                                                                                                                                                                                      CTAGTCCTCGTCGTCGCTGCTGGTATGCTCGGGACTGGCGGGCAGGGGGG 87
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o. 5844079
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                                                                                                                                                                                                                                                                                              Score 453.8; DB 3; Pred. No. 5.6e-92; O; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                   Length 1425;
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                 Sequence 5, Application US/08748591 Patent No. 5759811
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INFORMATION:
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-08-748-591-5
Sequence 5, Application US/08748591
Patent No. 5759811
GENERAL INFORMATION:
APPLICANT: Epstein, Ervin
APPLICANT: BOALIAS, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EDERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
APPLICATION: 435
COLASSIFICATION: 435
LATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J

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TELEPHONE: (415) 822-5070
TELEFAX: (415) 824-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches
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870 GCTCACCTGCTCTTTACGGCTGACAATCACACGGAGCCCGCAGCCCCGCTTCCGGGCCACA 929
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Local Similarity 70.9%;
les 630; Conservative
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                                           AAGAAGGTCTTCTACGTGATCGAGACGCGGGGAGCCGCGAGCGCCTGCTCACCGCC
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Pred. No. 1.3e-91;
0; Mismatches 253;
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REFERENCE/DOCKET NUMBER: 0651

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAN: (415) 854-0875

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA.
US-08-748-591-10
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Best Local
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APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1013 TCCTCGGGCTCGGGGCCCCTTCCGGGGGCGCACTGGGGCCTCGGGCGC
416 GAAGAAAACACCGGAGCGGACAGGCTGATGACTCAGAGGTGTAAGGACAAGTTGAACGCT
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CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    90 CTGGTCCTGTTGCTGCTGGTGGTGCCCGCGCATGGGGCCTGCGGGCCGGGTCGGGTC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                    GAGGAGAACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCG 389
                                                                                                                                              CCCAATGTGGCCGAGAAGACCCTAGGCGCCAGCGGAAGGTATGAAGGGAAGATCTCCAGA 355
                                                                                                                                                                                   AACTCCGAGCGATTTAAGGAACTCACCCCCAATTACAACCCCCGACATCATATTTAAGGAT 415
                                                                                                          AGCTCCGAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGAC 329
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Similarity 70.9%;
30; Conservative
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08176427B Patent No. 5789543 GENERAL INFORMATION:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,427E

FILING DATE: 30-DEC-193

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

AAME: VINCENT, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HMI-006
                                                                                                                                                                                                                                                                                                                        APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1013
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CITY: E
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                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTCGGGCTCGGGGCCCTTCCGGGGGCCCACTGGGGCCTCGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAAGGTCTTCTACGTGATCGAGACGCGGGAGCCGCGCGAGCGCCTGCTGACCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACCAGGGCCGGCTGCTCTACAGCGACTTCCTCACTTTCCTGGACCGCGACGACGGCGCCC 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGGCGGCACCAAGCTGGTGAAGGACCTGAGCCCCGGGGGACCGCGTGCTGGCGGCGGAC
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                                                                                                 US/08/176,427B
   900-IWH
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; LOCATION:
US-08-176-427B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 227-7400; INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1313 base -- 'Type"
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                                                                                                                                                                                                                                                                                                                                         391
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les 704; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                           CCACATCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCG
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                   TGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCG
                                                                                    AGGATGGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCCACAGGC
                                                                                                                                                                     GTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGG
                                                                                                                                                                                                                          ACTCGGCCGCAGCCAAGACGGGCGGCTGCCTGCCCGGAGCCCAGGTACGCCTGGAGA
                                                                                                                                                                                                                                                                                           GCTTTGACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGC
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AGAAGGTCTTCTACGTGATCGAGACGCTGGAGCCGCGAGCGCCTGCTGCTCACCGCCG
                                                                                                                                                                                                                                                                        GTTTCGACTGGGTCTACTATGAATCCAAAGCTCACATCCACTGTTCTGTGAAAGCAGAGA
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                                                                 ACCAGGGCCGGCTGCTACAGCGACTTCCTCACCTTCCTGGACCGCGACGAAGGCGCCCA
                                                                                                                                    AGGGCGGCACCAAGCTGGTGAAGGACTTACGTCCCGGAGACCGCGTGCTGGCGGCTGACG
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Pred. No. 1.1e-88;
0; Mismatches 357;
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US-08-356-060A-4
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US-08-356-060A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Applic Patent No. 5844079
                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,779
REFERENCE/DOCKET NUMBER: MMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                         TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1109
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1049
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                                           MOLECULE TYPE:
FEATURE:
                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989
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CITY: Boston
STATE: MA
COUNTRY: USA
           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435
                                                                                           STRANDEDNESS:
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                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                           both
                                                                                                                                                                        227-5941
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CCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCT 1092
                                                                                                               CATTIGCCAGCCAGCCIGGCCGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGC
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                                                                                                 TCTTTGCCAGCCGCGTGCGCCCCGGGCAGCGCGTGTACGTGGTGGCTGAACGCGGCGGGG
                                                                                                                                                  CGCACCTGCTCTTCGTGGCGCCCCACACGACTCGGGGCCCACGCCCGGGCCAAGCGCGC
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PCT-US95-02315-1
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GENERAL INFORMATION:
APPLICANT: Jessell
APPLICANT: Dodd, J
APPLICANT: Roelink
APPLICANT: Edlund,
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 706; Conserv
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1715 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0231
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APPLICANT: EGLUNG, THOMBER
TITLE OF INVENTION: DNA ENC
TITLE OF INVENTION: HEDGEHO
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
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CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 1036
ZIP: 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: John P. White REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 45 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
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ADDRESSEE: Cooper &
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ATTORNEY/AGENT INFORMATION:
NAME: John P. White
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                       463
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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AC 1110
                                      TGGTCCTGTTGCTGCTGGTGGTGCCCGGCGCATGGGGCCTGCGGGCCGGGTCGGGTGG 150
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                                                                                                    TGGGCAGCCGCCGCCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCC
                                                                                                                                                 TGGCCCTTGCTTCCTCGCTGCTGTGTGCCCCCGGACTGGCCCTGTGGGCCCCGGCAGGGGGT 405
                     CCAACGTAGCCGAGAAGACCCCTAGGGGCCCAGCGGCCGATATGAAGGGAAGATCACAAGAA
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1185 Avenue of the
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                                                                                                                                                                                                              Score 432; DB 6; Pred. No. 3.8e-87; 0; Mismatches 355;
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 Sequence 3, Application US/08176427B Patent No. 5789543
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: MCMAhon, Andrew P.
APPLICANT: Tabin, Clifford J.
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Ingham, Phillip I
McMahon, Andrew I
Tabin, Clifford
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STREET: 60 St CITY: Boston

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REFERENCE/DOCKET NUMBER: 4MI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.4 Matches 665; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: #33 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                        520 ACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACT
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                                                                                                                       CGGTGATGAACATGTGGCCCGGAGTACGCCTACGTGTGACTGAAGGCTGGGACGAGGACG
                                                                                                                                                                                                                                      CGGTGATGAACCAGTGGCCCGGTGTGAACCTGCGGGGTGACCGAGGGCTGGGACGACGACGA
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                                                                                      GCCACCACGCACAGGATTCACTCCACTACGAAGGCCGTGCCTTGGACATCACCACGTCTG
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Pred. No. 1.7e-84;
0; Mismatches 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embiritle OF INVENTION: Proteins and U.
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                  APPLICATION NUMBER: US/08, FILING DATE: 14-DEC-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08, APPLIC
                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1058
                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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USA
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30-DEC-1993
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                                                                                                                                                US/08/356,060A
                           US 08/176,427
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; NAME/KEY: ; LOCATION: US-08-176-427B-3

MOLECULE TYPE: FEATURE:

TOPOLOGY:

TYPE: nucleic acid STRANDEDNESS: both

Query Match

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 665; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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NAME: Vincent, Matthew P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
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TCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGC 879
                                                   GCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCT 819
                                                                                                                               GTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGAGGATGGGA 759
                                                                                                                                                                                                  CAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCCAGGTACGCCTGGAGAGTGGGGCGC
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                                                                                                                                                                                                                                                                                                                      ACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACT 579
                                                                                                                                                                                                                                                                                                                                                                                  GCCACCACTCAGAGGAGTCCCCTGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAG
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                                GAGTGGTACCCACGCCAGTGCTGCTCCTTCCTGGACCGGGATCTGCAGCGCCGCGCCCTCGT
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; LOCATION:
US-08-176-427B-9
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US-08-176-427B-9
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                                                                                                                                                                                                                                                                                                                             ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
SOSTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
                                                                                                                                          TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pair
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                       MOLECULE TYPE: FEATURE:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
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STATE: MA
                                                                                                        STRANDEDNESS:
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227-5941
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Best Local Similarity

25.8%;

Score 418.2; DB Pred. No. 4e-84;

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Length

Query Match

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TATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCC 644
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    CATTTGGCCTTCGCGCCCGCCAGGCTCTATTATTACGTGTCAT 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCATCGAGACTCAGGACCCCCCACGCCCCCGCCTGGCACTCACCCGCTCACCTGCTCTTT 884
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                                                                                                                                                                                                                                                                                                             CAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGC---AGCCTGCCGCGTG 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGACGGGCGGCTGCTTCCCTGCCGGAGCCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTG
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                                         CAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGGCAT 1164
                                                                                     ATTGTGGTCGACAGAATACTGGCGTCCTGTTACGCCGTAATAGAGGACCAGGGGCTTGCG
                                                                                                                                                                              CAGCGGATATACACGGAGGAGCAGCGGGGCTCGTTCGCACCAGTGACTGCACATGGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/176
APPLICATION NUMBER: US 08/176
FILING DATE: 30-DEC-1993
ATTORNET/AGENT INFORMATION:
NAME: V1ncent, Mathew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
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COMPUTER READABLE FORM:
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CITY: Boston
STATE: MA
345 GCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGGTG
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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Local Similarity 63.4%;
hes 674; Conservative
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TOPOLOGY: lir
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ZIP: 02109
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                                                                  AAGGAGCTCACCCCCAAITACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGC 344
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                                           AAAGAACTTACTCCAAATTACAATCCCGACATTATCTTTAAGGATGAGGAGAACACGGGA
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Pred. No. 4e-84;
O; Mismatches 383;
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Search completed: June 5, 2000, 07:56:48 Job time: 3779 sec

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Title:
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yent to reduce cerebra s can also be limited h recombines with the transcription regulate tration of the ptc the les against ischaemic coke (thrombolic or en ay also be used as a part or spinal cord, nyelitis, or in conjuntich may be prophylaction, cause cerebral hypound depletion, including uses CIV by at least; nce encodes a hedgehous	Location/Q 51. 1286 /*tag-a /product- 3387. 3387. 883556. Y INC. 98. 08. 08. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10	enti enti cDNA ptc 1 erebi farci	1256 1251 1251 1251 525 530 603 603 548 528 1416
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increasing the survival of neuronal, dopaminergic and GABA-nergic cells by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease

Sisclosure; Page 95-97; 138pp; English.

This nucleotide sequence comprises a coding region for the human comprises a coding region for the human standard by the findian hedgehog protein (see W97763). The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders for the general loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra.

Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans-activation
                                                                                                                                                                                                                                                                                                     Mahanthappa NK, Miao N, WPI; 99-142578/12. P-PSDB; W97763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Indian hedgehog (Ihh) cDNA.

Indian hedgehog; Ihh gene; human; dopaminergic; GABA-nergic; ptc therapeutic; patched; signal transduction; Parkinson's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                           04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
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21-MAY-1999
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Sequence 1622 BP; 277 A; 549 C; 510 G; 286 T;
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Human Indian hedgehog protein Ihh cDNA. Indian hedgehog; Ihh gene; human; hedgehog therapeutic; ptc therapeutic; patched; signal transduction; muscle a cachexia; muscular myopathy; myoblastic sarcoma; therap

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(first entry)

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Location/Qualifiers 51. .1286 /*tag= a

WO9910004-A2 04-MAR-1999.

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PS Disclosure; Page 104-106; 130pp; English.
PS Disclosure; Page 104-106; 130pp; English.
PS This nuclectide sequence comprises a coding region for the human CC Indian hedgehog protein Thh (see Y05516). The invention relates to CC tissue by ecotopically contacting muscle cells, especially muscle cC tissue by ecotopically contacting muscle cells, especially muscle cC tissue by ecotopically contacting muscle cells, especially muscle cC tissue by effect of hedgehog proteins on patched signalling, or cC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog proteins on patched signalling, or cC activates or potentiates patched signalling) in an amount effective CC to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or CC comsetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of mesole tissue such as in myoblastic or cc neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at CC least a bloactive extracellular portion of a hedgehog protein (see CC 905510-19) encoded by a vertebrate hedgehog gene (see X25098-107), CC especially a human hedgehog gene.

277 A; 549 C; 510 G; 286 T;
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Best Local Similarity
Matches 1622; Conserv
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29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hi
WPI; 99-243557/20.
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                   TGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGCCAATAAGTATG
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500	CACCAGCGTCCCCCACCCGCGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCG 1	1441	Qy
440	GGACACTGGCTCCTGCCATCTCCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGC 1	1381	рь
440	GACACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGC 1	1381	Qγ
380	ACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGG 1	1321	뫄
380	CTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGG 1	1321	Qy
320	TGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTGGAACTGCTGT 1	1261	ДĎ
320	GGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTGGAACTGCTGT 1	1261	Qy
260	CCACCCAC 1	1201	Db
260	CCCCAGCTGCTCTACCGCCTGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCAC	1201	Qy
200	TGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGT 1	1141	Db
200	GAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGT 1	1141	Qγ
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140	GGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCCTTCTGGCCCC 1	1081	Qy
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080	GGCCCTCGGGGCCTACGCCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGG 1	1021	VΩ
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00	GGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCACGTGCAGCCTGGCCAGT	901	Qy
00	ACCCCCCACGCCTGGCACTCACACCCGGTCACCTGCTTTTACGGCTGACAATCACA 9	841	фd
00	CCCCCACGCCGGCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCTGACAATCAC	841	Qy
40	TCATTTTCCTGGACCCCCACACGCCTGAGAGCCCTTCCAGGTCATCGAGACTCAGG 8	781	ДD
40	CATTITCCIGGACCGCGAGCCCCACAGGCTGAGAGCCTTCCAGGTCATCGAGACTCA	781	Qy
80	GCCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGC 7	721	рb
80	GCCGGGAGACCCGTGTGCTGGCCATGGGGGAGGAGGATGGGAGCCCCACCTTCAGCGATGT	721	Qy
20	TCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCTTGTCAGCCGTGA 7	661	ర్థ
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ō	CCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACGGCCGCTGCT 6		дь .
60	CCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGC	601	οv
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00	ACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTACGAGTCAAA	541	Qy

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1621 CC 1622

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DR P-PSDB; W94470.

Proditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks pisclosure; Page 66-68; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by ischaemic conditions by administering a ptc (patched) conditions by administering a ptc (patched) concerned to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic or injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The coronant sequence encodes a hedgehog sequence given in the present coronance conditions.
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07-JAN-1999.
26-JUN-1998; [
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Mouse Inh hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

brain infarction; cerebral infarction; transient ischaemic attack;

stroke; cerebral infarct volume; spinal cord; oedema; trauma;

stroke; cerebral infarct volume; spinal cord; oedema; trauma;
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WPI; 99-095458/08.
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(ONTO-) ONTOGENY INC.
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                                         CTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCTTCAAGGAG
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PA (ONTO-) ONTOGENY INC.

DR WP1; 99-142578/12.

DR WP1; 99-142578/12.

DR P-SSDB; W97767.

PT Increasing the survival of neuronal, dopaminergic and GABA-nergic processing the survival of neuronal, dopaminergic and GABA-nergic process.

PT Increasing the survival of neuronal, dopaminergic and GABA-nergic process.

PT the treatment of parkinson's disease process in the treatment of parkinson's disease process.

PT the treatment of parkinson's disease process in the finding that hedgehog proteins are useful as protective agents on the finding that hedgehog proteins are useful as protective agents on the finding that hedgehog proteins are useful as protective agents on the general loss of tissue from the substantia nigra.

CC In the treatment and grophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra.

CC or the general loss of tissue from the substantia nigra.

CC disease (both claimed), amyotrophic lateral sclerosis and cerebral constructs of both claimed), amyotrophic lateral sclerosis and cerebral cc disease (both claimed), amyotrophic lateral sclerosis and cerebral cc dischapentics (i.e. egents which minic the effect of naturally cc encoding recombinant hedgehog polypeptides and trans-activation cc constructs for altering hedgehog polypeptides and trans-activation cc constructs (i.e. agents which minic the effect of naturally cc constructs (i.e. agents which minic the effect of naturally cc constructs (i.e. agents which minic the effect of naturally cc constructs (i.e. agents which minic the effect of naturally cc and in the implantation of such neuronal cells in an analysing trom the used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the process of the process of the process of certain drugs, and in the conditions arising from the use of certain and an analysing treatment of hypoxia, e.g. as a neuroprotective cc.
                                                                                                                                                                                                                                                                                                                          Query Match 63. Best Local Similarity 88. Matches 1129; Conservative
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Mouse Indian hedgehog (Ihh) cDNA.

Indian hedgehog: Ihh gene; mouse; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's d
ptc therapeutic; amyotrophic lateral sclerosis;
Huntington's disease; amyotrophic lateral sclerosis;
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X07273;
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04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
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CC This nucleotide sequence comprises a coding region for the mouse CC Indian hedgehog protein Ihh (see Y05512). The invention relates to CC a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle CC stem/progenitor cells, in vitro or in vivo, with a hedgehog CC therapeutic (i.e. hedgehog polypeptides and gene therapy CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog proteins on patched signalling, or CC constructs or potentiates patched signalling in an amount effective to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be cCC muscle atrophy, cachexia, or musculat myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic growth of muscle tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at cleast a bioactive extracellular portion of a hedgehog protein (see Y05510-9) encoded by a vertebrate hedgehog gene (see X25098-107), cespecially a human hedgehog gene.

Sequence 1281 BP; 229 A; 401 C; 393 G; 258 T;
                                                                                                                                                                                                                                                                                                                        Query match
Best Local Similarity
Matches 1129; Conserv
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Indian hedgehog; Ihh gene; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-24357/20.
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04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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                                                                       CTCACCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACACAGGCGCCGAC
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Human Indian hedgehog protein gene. Human; Indian hedgehog gene; nested polymerase
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18-MAR-1996
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therapy.

Therapy.

Claim 4; Page 146-47; 210pp; English.

CC The sequence encodes a human Indian hedgehog protein, homologous

CC The sequence encodes a human Indian hedgehog protein (R77337), and has been isolated by

CC to a Drosophila hedgehog protein (R77337), and has been isolated by

CC screening of human genome DNA by nested polymerase chain reaction

CC using primers Q91643, Q91644 and Q91645, followed by use of a clone

CC to screen a human fetal lung 5'-stretch plus CDNA library in phage

CC lambda gt-10. Probes and primers derived from hedgehog sequences

CC may be used as diagnostic agents for neuromuscular, autonomic or

CC central nervous system disorders, and the gene may also be used in

CC gene therapy. Antibodies generated from the encoded protein may be

CC used as therapeutic or research reagents.

SQ Sequence 939 BP; 154 A; 305 C; 314 G; 166 T;
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Best Local Similarity 100.
Matches 936; Conservative
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W09518856-A1.

13-JUL-1995.

30-DEC-1994; U14992.

30-DEC-1994; US-176427.

14-DEC-1994; US-356060.

(HARD) HARVARD COLLEGE.

(IMCR) IMPERIAL CANCER RES TECHNOLOGY.

Ingham PW, Mcmahon AP, Tabin CJ;
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WPI; 95-255060/33.
P-PSDB; R77344.
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system disorder(s) and in gene
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276 GAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAG

Query Match Best Local Sin Matches 928;

Similarity

52.0 ilarity 88.2 Conservative

3.2%;

Score 843.2; DB 1; Pred. No. 1.3e-157; 0; Mismatches 123;

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13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1994; US-176427.

14-DEC-1994; US-356060.
(HARD) HARVARD COLLEGE.
(IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
WPI; 95-255060/33.
P-PSDB; R77343.
P-PSDB; R77343.
Hedgehog-like protein(s) and nucleic acide treat degenerative nervous system discontinuous control of the 
The sequence encodes a mouse Indian hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and has been isolated by low stringency screening of a mouse genome DNA library and screening of an 8.5 day post coitum cDNA library. The partial cDNA is complete at the 3'-end, as evidenced by the presence of a polyadenylation consensus sequence and short poly-A tail. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

Sequence 1056 BP; 204 A; 321 C; 312 G; 219 T;
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Q91640;
14-MAR-1996
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Mouse; Indian hedgehog gene; probe; primer; diagnostic;
nervous system disorder; gene therapy; antibody; ds.
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Matches 763;
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P-PSDB; R77338.
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30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
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Q91636;
22-FEB-1996 (first ent
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Claim 2; Page 133-35; 210pp;
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63; Conservative
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                          WO9900117-A2.
07-JAN-1999.
26-JUN-1998; U13387.
27-JUN-1997; US-883656.
(ONTO-) ONTOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1999 (first entry)
Chicken Shh hedgehog cDNA sequence.
Chicken Shh hedgehog cDNA sequence.
Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell; brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord; oedema; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X16182 standard; cDNA; 1277
X16182;
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Proditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks proceeding infarction, stroke and transient ischaemic attacks.

PS Disclosure; page 63-64; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by cischaemic or epoxic conditions by administering a ptc (patched) construct which recombines with the genomic hedgehog gene to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic njury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic cattacks. It may also be used as a prophylactic in many qther cases of a tacks. It may also be used as a prophylactic in many qther cases of conditions may cause cerebral hypoxia, or progressive loss of neurons conditions may cause cerebral hypoxia, or progressive loss of neurons conduction with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,8. The consent conduction condens a hedgehog sequence given in the present
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Best Local Similarity
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Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase rinhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease placetosure; page 83-85; 138pp; English.

This nucleotide sequence comprises a coding region for the chicken Sch Sonic hedgehog protein (see W97765). The invention is based on the finding that hedgehog proteins are useful as protective agents comprises of neurodegenerative disorders comprises of neurodegenerative disorders consuling from the loss of dopaminergic and/or GABA-nergic neurons, cor the general loss of tissue from the substantia nigra.

Exemplary disorders include parkinson's disease, Huntington's cliscase (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken Sonic hedgehog (Shh) cDNA.
Chicken Sonic hedgehog (Shh) cDNA.
Sonic hedgehog; Shh gene; chicken; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's disease;
Huntington's disease; amyotrophic lateral sclerosis;
cerebral ischaemia; hypoxia; neuroprotective; gene therapy; ss; ds.
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24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
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P-PSDB; W97765.
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-GTACGTGCTGGTGGCTGCCAGGCC

984 886 930

-CAGCCCGCTTCGGGGCCACAT

822

706

646 702 586 642 526

766

582 466 406

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occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human IAh and Dhh polypeptides (see W97063-64) are preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can also be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective
                                                                                                                                                                                                                                                                                                                                                     constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of natural
                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding recombinant hedgehog polypeptides and trans-activation
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262 A;
396 C;
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Length 1277;

Conservative

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360;

Indels

48;

Gaps

4

166 222 28.3%;

Score 459; DB 1; Pred. No. 3.9e-82; Mismatches

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cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cariatac muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-derived tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bloactive extracellular portion of a hedgehog protein (see Y05510-19) encoded by a vertebrate hedgehog gene (see X25098-107), especially a human hedgehog gene.

Sequence 1277 BP; 262 A; 396 C; 387 G; 232 T;
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 92-94; 130pp; English.

This nucleotide sequence comprises a coding region for the chicken Sonic hedgehog protein shh (see Y05510). The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that the constructs of the therapeutic (i.e. a small organic molecule that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1999.
04-MAR-1999: U17922.
28-AUG-1998: U17922.
29-AUG-1997: US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, Ingham PW;
WPI; 99-243557/20.
                                                                                                                                                                                                                                                    mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or
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Sonic hedgehog; Shh gene; chicken; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new method to regulate muscle growth
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Query Match

28.3%;

Score 459;

DB 1;

Length 1277

Qy	Ф	Ф	D Qy	g qq	p S	Qу	g Qy	D Qy	ОУ	β Q	Qy Bb	P Q	DP QA	p Q	Db Db	Оу	dp Qy	ж ма
1162	1102 1067	1042	985 947	931 887	883 827	823 767	763 707	703 647	643 587	583 527		463 407	403 347	343 287	283 227	223 167	163	st Lo
CATGGGGCAGCTGGACCCCGGGGGAGGTGTGC 1	TGGCTGACCACCACCTGGCTCAGTTGGCCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG 1	CCCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG 1	TGCAGCCTGCCGCGTGGCAGCTGTCTACACACGTGGCCCTCGGGGCCTACGCCC 1	TTGCCAGCCAGGTGCAGCCTGGCCAGTACGTGGTGGCTGGGTGGCAGGCC 9	TTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCACAT 9	AGGTCATCGAGACTCAGGACCCCCACGCCGCTGGCACTCACACCCGCTCACCTGCTCT 8	CCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCTTCC 8	TGGCCTTGTCACCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCC 7	CCAAGACGGGGGGCTGCTTCCCTGCCGGAGGCCCAGGTACGCCTGGAGAGTĠGGGGGGGGTG 7	TGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAG 6	GCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTTGACTGGG 5	ACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGGGGGGACATCACCACATCAGACC 5	TGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCC 4	GCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCTCGG 4	TCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGGAGAACACAG 3	AGAAGACCCTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGC	GGCGACCGCCACACTCGTGCCGCCTGCCTACAGCAGTTCAGCCCCAATGTGCCCG 2	cal Similarity 65.2%; Pred. No. 3.9e-82; 763; Conservative 0; Mismatches 360; Indels 48; Gap
194	161 126	101	041 006	46	86	26	66	62 06	02	42 86	26 8	22	06 2	02	6 4 6	82	6 2 2	ΣĎ.

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RESULT TO THE PROPERTY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                       PT Increasing the survival of neuronal, dopaminergic and GABA-nergic process of the survival of neuronal, dopaminergic and GABA-nergic process. By using a ptc therapeutic such as a protein kinase prinhibitor, or an agent derived from hedgehog polypeptides, useful in process. This nucleotide sequence comprises a coding region for the human CC Dhi Desert hedgehog protein (see W97764). The invention is based on the treatment and prophylaxis of neurodegenerative disorders come the finding that hedgehog protein sare useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders consulting from the loss of dopaminergic and/or GABA-nergic neurons, constituting from the loss of dopaminergic and/or GABA-nergic neurons, constituting from the loss of tissue from the substantia nigra.

CC disease (both claimed), amyotrophic lateral sclerosis and cerebral schemals. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs constructs for altering hedgehog gene regulatory sequences) and constructs of ratering hedgehog gene regulatory sequences) and coccurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. A bloactive constructs constructs are products can also be used for the maintenance of constructs in an animal. They can also be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, confidence of the conditions arising from the use confidence.
                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahanthappa NK, Miao N, WPI; 99-142578/12. P-PSDB; W97764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
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                                                  GCCGCTATGCGCGCAAGCAGCTCGTGCCGCCTACTCTACAAGCAATTTGTGCCCGGCGTGC
                                                                                                                                                                                                                                                                                     Similarity
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e 1190 BP; 176 A;
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CC This nucleotide sequence comprises a coding region for the human CC Desert hedgehog protein Dhh (see Y05517). The invention relates to CC a method for modulating the formation and/or maintenance of muscle CC stem/progenitor cells, in vitro or in vivo, with a hedgehog cC therapeutic (i.e. hedgehog polypeptides and gene therapy CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog polypeptides and gene therapy CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog proteins on patched signalling, or CC constitutes or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or CC consetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The compoliastic growth of muscle tissue such as in myoblastic or mephlastic or muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at CC (ease at a bloactive extracellular portion of a hedgehog protein (see CC 905510-19) encoded by a vertebrate hedgehog gene (see X25098-107), CC especially a human hedgehog gene.

SQ Sequence 1190 BP; 176 A; 375 C; 424 G; 215 T;
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Matches
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Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Desert hedgehog protein Dhh cDNA.

Desert hedgehog; Dhh gene; human; hedgehog therapeutlc;
ptc therapeutlc; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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WO9910004-A2.
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                                                                                          sapiens.
GCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGGGGGGACATCACCACATCAG
                                                                                                                                                                                            GCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACA 339
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Pred. No. 4.1e-81;
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30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD) HARVARD COLLEGE.
(HARD )
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                                                                               Homo sapiens.
WO9518856-A1.
                                                                                                                         Human; sonic hedgehog gene; nested polymerase chain reaction; fetal lung; probe; primer; diagnostic; nervous system disorde
                                                                                                                                                     Human sonic hedgehog protein
                                                                                                                                                                                 Q91639 standard; cDNA; 1425
Q91639;
                                                                                                           gene therapy; antibody;
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RPI; 95-25506(0/33.

RP-PSDB; R77341.

RP-PSDB; R77341.

RP-PSDB; R77341.

RP-PSDB; R77341.

Redgehog-like protein(s) and nucleic acid(s) encoding them - useful to treat degenerative nervous system disorder(s) and in gene therapy.

PT therapy.

PT therapy.

PT claim 2; Page 143-45; 210pp; English.

CC laim 2; Page 143-45; 210pp; English.

CC using primers of human genome DNA by nested polymerase chain reaction using primers 091643, 091644 and 091645, followed by use of a clone to screen a human fetal lung 5'-stretch plus cDNA library in phage to screen a human fetal lung 5'-stretch plus cDNA library in phage clambda-gri0. A clone has been isolated from a phage P1 library by polymerase chain reaction, using primers SHHPC (091655) and SHR (091655) to give clone SHHP1. A 2.5-kb EcoRI CA repeat fragment is amplified using primers SHHPL. A 2.5-kb EcoRI CA repeat fragment is amplified using primers SHHPL. A 2.5-kb EcoRI CA repeat fragment crosses and primers derived from the sonic hedgehog sequence may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

Sequence 1425 BP; 249 A; 461 C; 506 G; 206 T;
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Best Local Similarity
Matches 631; Conserv
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AA064660 LOCUS DEFINITION ACCESSION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS		4444 444 442 442 442			222222221117 2222222222227 876543210987		
AA064660 314 bp zml3f08.sl Stratagene IMAGE:52543 3' simila PRECURSOR. ;, mRNA see AA064660 GI:1558743 EST. human. Homo sapiens Eukaryota; Metazoa; Ch Eutheria; Primates; Ca (bases 1 to 314) Hiller L. Lennon, G. Chissoe, S., Dietrich, Mardis, E., Moore, B., Nonhifing, T., Schellent Trevaskis, E., Underwoe and Marra, M.		4444	44444	***************************************			Match 21.3 20.1 19.7 14.5 10.2
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od, ita	ALIGNMENTS						
mRNA EST 23-DEC-1997 ncreas (#937208) Homo sapiens cDNA clone to TR:G443942 G443942 DESERT HEDGEHOG nce. data; Craniata; Vertebrata; Mammalia; rrhini; Hominidae; Homo. pecker.M., Bonaldo.M.F., Chiapelli,B., DuBuque.T., Favello,A., Gish.W., Kucaba.T., Lay.M., Le,M., ris,M., Parsons,J., Prange,C., Rifkin,L., ris,M., Parsons,J., Tan,F., Thterry.Meg,J., g,K., Soares,M.B., Waterston,R., Wilson,R.		AL077488 Drosophil AL166750 Drosophil B10823 T11E7-T7 TA AQ895529 HS 4832 A AL078276 Drosophil	AL098770 Drosophil AL105068 Drosophil AL108768 Drosophil AL050923 Drosophil AL055652 Drosophil	AL098882 Drosophil AL098882 Drosophil AL104949 Drosophil AL065629 Drosophil AL0659794 Drosophil AL063912 Drosophil AL101589 Drosophil	AL066051 Drosophil AL09352 Drosophil AL054280 Drosophil AL078875 Drosophil AL106054 Drosophil AL106054 Drosophil AL106054 Drosophil AL106054 Drosophil AL106054 Drosophil AL106058 Drosophil AL106648 Drosophil AL106683 Drosophil AL104440 Drosophil AL104440 Drosophil AL104440 Drosophil	AL10855 Drosophil AL053013 Drosophil AA245525 my52c03 r AI325370 mi34bil.y AA032692 mi34bil.r AL066051 Drosophil AL106460 Drosophil AL066742 Drosophil AL053013 Drosophil	Description AA064660 zm13f08.s AI645932 mu11g06.y AI666359 mu11g06.x AW144802 EST291875 AI958076 fc90e01.y AL066742 Drosophil AI015155 ot70h05.s
Qy 953 GGGAGGAGCCG Qy 1013 ATGTCCTGGCCT Qy 1013 ATGTCCTGGCCT Db 181 ATGTCCTGGCCT Qy 1073 CCCCCTTGAGAC Qy 1073 CCCCCTTGAGAC Qy 1133 CTGGCATGCATT Db 241 CCCCCTTGAGAC Qy 1133 CTGGCATGCATT Db 299 CTGGAATGCATT Db 299 CTGGAATGCATT A1645932 A1645932 DEFINITION mullg06.y1		Matches 285; Conse	н	BASE COUNT 31 a	Possible r Insert Len Seq primer High quali FEATURES 1	Email: est WARNING: T plate of t Thus, the kept in mi This clone IMAGE CONS	TITLE Generation JOURNAL Genome Res MEDLINE 97044478 COMMENT On May 9, Contact: Washington 4444 Frax: 314 2 Fax: 314 2

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AI645932 537 bp mRNA EST 29-APR-1999 mullg06.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:639130
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/db_xref="GDB:3916972"
/db_xref="TGDB:3916972"
/db_xref="Tdaxon:9606"
/clone="Ib="Stratagene pancreas (#937208)"
/clone=lib="Stratagene pancreas (#937208)"
/lab_host="SOUR cells (Kanamycin resistant)"
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ity 91.3%;
servative
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                                                                                                                                                                                                                                                                                                                                                                                                  TT 310
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There is evidence that suggests that the 384-well parent
this clone contains both human and mouse derived clones.
e origin of this clone is uncertain. This caution should be
mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on University School of Medicine
est Park Parkway, Box 8501, St. Louis, MO 63108
286 1800
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Pred. No. 2.8e-40;
0; Mismatches 25;
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Best Local Similarity 86.8
Matches 263; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the second contact of the second contact the seco
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On May 18, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Eukaryota; Metazoa;
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Location/Qualifiers
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1 (Dases 1 to 537)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
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; Pred. No. 2.6e
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mullg06.x1 Soares_thymus_2NbMT
3' similar to TR:Q61488 Q61488
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On May 18, 1998 this sequence version
Other_ESTs: mullg06.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this ned
data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand High quality sequence stop: 261.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 463)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AI666359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI666359.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537
                                                                                                                          Conservative
                                                                                                                                                                                                                      87
                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .463
                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:4804713
                                                                                                                                       19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                          0;
                                                                                                                                       Score 234.8; DB 4
Pred. No. 1.6e-36;
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus cDNA clone IMAGE:639130 DESERT HEDGEHOG HOMOLOG PRECURSOR;
                                                                                                                                                       DB 49;
                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replaced gi:3136856
                                                                                                                          Indels
                                                                                                                                                       Length
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                                                                                                                                                         463;
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DEFINITION
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                                                                                                                                                                       Query Match
Best Local S
Matches 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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297 GACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCCGTGATGAACATGTGGCC 356
                                                                      237
                                                                                                                      177 CAGTGGGCCAGCGGAGGGGAGGGTGGCAAGGGGCTCCGAGCGCTTCCGGGACCTCCTTGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
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                                     61
                                                                                                                                                                                         Local Similarity
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                                                                                                    CAGCGGGCGCTACTAAGGCAAAATCGCGCGCAGCTCTGAGCGCTTCAAGGAGCTCACCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCCTCTGCTATACAAGCAGTTTGTGCCCCAGTATGCCCCGAGCGGACCCTGGGCGCGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCCAGCGGAGCGGAACGTAACAAGGGGGTCGGAGCGCTTCCGGGGACCTCGTACCCAAC
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                                                                                                                                                                       220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockvi.
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nhiee@tigr.org
For clone availability, additional sequence and expression
Information related to this EST please check the TIGR Rat (
Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a cl
contact the ATCC (http://www.atcc.org/atcc.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 29)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quacker Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW144802 299 bp mRNA EST291975 Normalized rat embryo, RGICG52 5' end similar to Indian AW144802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
On Jun 5, 1998 thi
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EST.
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                                                                                                                                                                                                                                                                            78
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                /organism="Rattus sp."
/db_xref="raxon:10118"
/db_xref="taxon:10118"
/clone="hgriG52"
/clone_lib="Normalized rat embryo, Bento Soares"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                M13 Reverse
                                                                                                                                                                                       14.5%;
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                                                                                                                                                                       0
                                                                                                                                                                                       Score 172.6; DB 6
Pred. No. 1.7e-24;
                                                                                                                                                                         Mismatches
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hedgehog protein, mRNA sequence.
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                                                                                                                                                                       Indels
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ACCESSION
VERSION
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AI958076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TTTACACTATGAGGGCCGCGCGGTGGATATCACCACCTCAGACCGCGACCGAAATAAGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Reopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 406)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.,

Waterston, R. and Wilson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  washU Zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced g1:3188836.
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A1958076 406 bp mRNA fc90e01.y1 Zebrafish WashU MPIMG TR.Q92008 Q92008 VHH-1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity Seq primer: T3 ET from Amersham H1gh quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI958076.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RessourcenZentrumPrimarDatenbank, Berlin, Germany (web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: zbrafish@watson.wustl.edu
stage embryos"
/lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib*"Zebrafish WashU MPIMG
/sex-"mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                        /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocati
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EST Danio rerio cDNA 5' simii
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RESULT
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                                         Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutvyo Osoegawa and haron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
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Location/Qualifiers
1. .932
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nes 144; Conservative 10
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      AI015155 459 bp mRNA EST 27-AUG-1998 ot70h05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622169 3' similar to TR:Q98938 Q98938 INDIAN HEDGEHOG
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 459)
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                          PROTEIN. ;, mRNA sequence.
                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                         Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the control of the description of the constructed in the control of th
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191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVSSGSGSGSVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGGCCGTCCAGCCGACTGGCATGCATTGGTACTCTCGGCTCCTCTACCGCTTAGCGGA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVGTSSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGS 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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              Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 512)

1 (bases 1, to 512)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                      my52c03.rl Barstead clone IMAGE:699460
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WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-98"
/clone="BACR19D16"
/note="end : TET3"
a 61 c 61 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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15.5%; Pred. No. 0.
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5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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                                                                                                                                                                                                                                                                                                                                                      EST 10-MAR-1997 organs MPLRB4 Mus musculus cDNA TR:G443944 G443944 INDIAN HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 82;
0.00017;
nes 132;
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                                                                                            CATCTGGCTCAGTTGGCCTTCTGCCCTGCGA 299
                                                                                                                                                                                                                                                                                                                       CATGGGACACTTGTGGTGGAGGATGTGGTGGCCTCCTGCTTTGCAGCTGTGGCTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCGCCGGCTACGCGCTGGGGACTCGGTGCTGGCGCCCGGCGGGGATGCGCCTTCGGCCA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCTGCTCTTCATTGCGGACAATCATACAGAACCAGCAGCCCACTTCCGGGCCACATTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144;
                                                                                                          AI325370 452 bp mRNA EST 23-DEC-1998 mi34bl1.yl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:465405 5' similar to TR:Q61724 Q61724 INDIAN HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
On Apr 14, 1993 this sequence version replaced Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                     PROTEIN ;, mRNA sequence. AI325370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28m13 rev2 ET from
High quality sequence stop: 511.
Location/Qualifiers
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Fax: 314 286 1810
Mus musculus
               house mouse
                                                     AI325370.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:699460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                     GI:4059799
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Pred. No. 0.00044;
0; Mismatches 127
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                                                                             121
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181 CTGCGACTGTTTCCC 195
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                     TTGAGACTGCTGCAC 1092
                                                                                                                                                  GTGGCCCTTGGGTCCTATGCTCCTCTCACAAGGCATGGGACACTTGTGGTGGAGGATGTG 120
                                                                             GTGGCCTCCTGCTTTGCAGCTGTGGCTGACCACCATCTGGCTCAGTTGGCCTTCTGGCCC
                                                                                                   CTGGCCTCTTGCTACGCGGTTCTGGAGAGTCACCACTGGGCGCACCGCGCTTTTGCCCCCC 1077
                                                                                                                                                                                        On Jan 19, 1998 this sequence version replaced g1:21522:
Contact: Marra //Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 452)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                        Similarity
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314 286 1810
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:465405"
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                                                                                                                                                                                                                                                                                                       Score 67; DB 44; ]
Pred. No. 0.00061;
0; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                              DB 44; Length 452;
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958 GAAGCCGTGGGCGTGTTCGCGCGCCCCCCCACGGGACGCTGCTGCTGAACGATGTC 1017

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 898 GTGCTGGCGCCGGGGGATGCGCTTCGGCCAGCGCGCGTGGCCCGTGTGGCGCGGGAG 957
                                                          Local Similarity
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AA032692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On NOV 29, 1993 this sequence version replaced gi:637531.
Contact: Marra M/Mouse EST Project
Washin-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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Seq primer: -28M13 rev2 from Amersham
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                      49
                                      Conservative
                                                                                                                                                                       M.Fatima Bonaldo.
96 c 100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:465405"
                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="unknown"
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                                                        58.5%;
                                      0;
                                                        Score 65.4; DB 2
Pred. No. 0.0011;
                                        Mismatches
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                                      Indels
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Mus.
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                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be coation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTGCCCCC
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 CGCGCCGSCSCGCCGGCSGGCCSGGCGSSGCGGCSGCCGSSCCGCSGKSKCGCGCGS
                                                                                                GGTGTTCGCGCGCCGGCTACGCGCTGGGGGACTCGGTGCTGGCGCCCCGGCGGG----GATG
                             CGCTTCGGCCAGCGCGCGTGGCCCGTGTGGCGCGGAAGCCGTGGGCCGTGTTCGCGC
                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)
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GSS.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fr
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                                                                                                                                                                                                                                                                                                /organism="Drosophila m
/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone_"BACR14N09"
/note="end : T7" .
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32.3%;
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ASBSSSSSSSSSTSTTBSTSBBBSTSSSSSGSSSSSBBSTBSBSSBTBTTTTTBTKSTS
                                                                                                                                                                                                l Similarity
73; Conserv
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GSS.
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                                                                                                                                                                                                                                                                                              /clone_lib="DrosBAC"
/clone="BACN37L08"
/note="end : SP6"
a 176 c 160 g
                                                                                                                                                                                                                                                                                                                                                                /plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila
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15.6%;
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1040 TGGAGAGTCACCAGTGGGCGCACCGCGCTTTTGCCCCCCTTGAGACTGCTGCACGCGCTAG 1099
844 GCGCCAGGCGACTTTGCACCGGTGTTCGCGCGCCGGCTACGCGCTGGGGACTCGGTGCTG 903
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                                                                                                                                                                                                                                                                                         724 TTCCTGGACCGGGACTTGCAGCGCCGGGCTTCATTTGTGGCTGTGGAGACCGAGTGGCCT 783
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                                                                        GCGSCGCSGCGCCGCCCSCCCCSCCCSSSSCGSSCCSSCCSSCCSSSCCSSGCCC
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37LO8 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 83;
Pred. No. 0.0045;
06; Mismatches 18
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                                                                                      Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPOI-98 and was constructed by partial EcoRI digestion of Drosophila bNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and by to order individual BAC clones, the entire library or and by the order individual BAC clones, the entire library or and by the order individual BAC clones, the entire library or and by the order individual BAC clones.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 932)
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AL066742.1 GI:4945205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1 (bases 1 to 512)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                   AA245525 512 bp
my52c03.rl Barstead r
clone IMAGE:699460 5'
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55 ot70h05.s

59 mul1906.y

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13 Drosophil

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160 Drosophil
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nes 417; Conserv
                                                                                                                                      GCAGCTGGACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGC
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                                                 GGGACTCTAACCACTGCCCTCCTGGAACTGCTGTGCTGGATCCAAAGGCCTCCTCACCAG
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                                                                                           AGGACTC-CACCGCTGCCCTCCTGGAACTGCTGTACTGGGTCCAGAAGCCTCTCAGCCAG
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This clone is available royalty-free th
IMAGE Consortium (info@image.llnl.gov)
MGI:433020
Seq primer: -28ml3 rev2 ET from Amersha
High quality sequence stop: 511.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:699460"
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les 372; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jan 19, 1998 this sequence version replaced Contact: Marra M/MOUSE EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:279221
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct orientation)
Seq primer: -40RP from Gibco
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 452)
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AI325370.1 GI:4059799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 415.
Location/Qualifiers
                           Conservative
                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:465405"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="unknown"
                                                      19.9%;
85.3%;
                                       0
                                     Score 323.2; DB 44;
Pred. No. 3.9e-54;
0; Mismatches 63;
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                                                                                                                                                                                                                 correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 390.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-Merck EST project

This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1133383.
Other_ESTs: z178b12.x5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI733725 435 bp mRNA EST 1
2178b12.y5 Stratagene colon (#937204) Homo sapiens
IMAGE:510719 5', mRNA sequence.
AI733725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 435)
/clone_lib="Stratagene colon (#937204)"
/tissue_type="tumor"
/cell_line="T84 carcinoma cell line"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:510719"
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3843214"
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                                                                                                                                                                                                         Waterston, R.
The MashU-HHMI Mouse EST Project
Unpublished (1996)
On Nov 29, 1993 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 324)
1 (bases 1 to 324)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA032692 324 bp mRNA EST 22-AUG-1996 m134b11.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:465405 5' similar to PIR:C49425 C49425 Indian hedgehog protein mouse; mRNA sequence.
                                                                                                                                              4444 Forest Park Parkway, Box 8501, St.
Tel: 314 286 1800
Fax: 314 286 1810
                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free ti
MAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA032692
AA032692.1
                  Possible reversed clone: similarity on wrong Seq primer: -28M13 rev2 from Amersham
               primer:
quality sequence stop: 98
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a 1 0 c 123 g 95 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                1140
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                                                                                                                                                                                                                                                                                                                                      Rattus sp. Rattus sp.
                                                                                                      AW144802.1
EST.
Eukaryota; Metazoa; Chordata; Craniata; Verte Eutheria; Rodentia; Sciurognathi; Muridae; M. 1 (bases 1 to 299)
Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (
                                                                                                                             AW144802 299 bp mF
EST291875 Normalized rat c
RGICG52 5' end similar to
AW144802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism≖"Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:465405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="Soares mouse embryo NbME13
                                                                                                                   GI:6161619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.5%;
                                                  Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 252; DB 27;
Pred. No. 3.3e-40;
D; Mismatches 45;
                                                                                                                                           mRNA
it embryo,
to Indian
                                                                                                                                         Bento Soares Rattus sp. cDNA clo
hedgehog protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
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  (REST) Catalog
                           Quackenbush, J.,
                                                                                                                                                                     30-OCT-1999
                                                     Mammalia;
Rattus.
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Best Local S
Matches 267
 TITLE
JOURNAL
                                                                                                                                             AUTHORS
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On Jun 5, 1998 this sequence version replaced gi:3189461.

Contact: Lee, NH

ATCC

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529
Fax: (301)-838-0208

Email: nhlee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a clone
contact the ATCC (http://www.atcc.org/atcc.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGCGGCCGACCGCCTCAT 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267;
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)

Hillier_L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Chissoe,S., Dietrich,N., Kucaba,T., Lacy,M., Le,M., Le,N., Havkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                    AAU99745 464 bp mRNA
2178b12.r1 Stratagene colon (#937204)
IMAGE::10719'5', mRNA sequence.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                      AA099745
AA099745.1 GI:1645856
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Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996)
                                     and Marra, M.
                                                                                                                                                                                                                                     numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGICG52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pt7T3Pac site_1: EcoRI; Site_2: NotI"
/note="Vector: pt7T3Pac site_1: EcoRI; Site_2: NotI"
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0; Mismatches
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2.2e-39;
32;
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              expressed
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Best Local Similarity
                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                       ACCTTG-AGGCTGGCACGGCGACTCCCAACTC-AGCCTGCTCTCACTACGAGTTTTCATA 1590
                                                                                                                                                                                                                                                          TACTCTTGCCTCC
                                                                                                                                                                                                                                                                                                CTCTGCCTCCCCC 1603
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                                                                                                                                                                                                                                                                                                                                      ACCTTGAAGGCTGGCACGGCGACTCCCAACTCAAGCCTGCTCTCACTACGAAGTTTTCAA
                                                                                                AW430605 291 bp
70323 MARC 4BOV Bos t
AW430605
AW430605.1 GI:696191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1974  Std Error: 0.00
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 221.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97044478
On Sep 12, 1996 this sequence version replaced
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                              Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Cell_line="T84 carcinoma cell line"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhOI; Cloned unidirectionally. Primer:
Gligo dT. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-Zap xR Vector; ~5' adaptor
sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTITTTTTTTTTTTTTTT 3'"

a 135 c 124 g 108 t 4 others
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/tissue_type="tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:510719"
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/db_xref="GDB:3843214"
                                                                                                                                                                                                                                                          310
                                                                                                  GI:6961912
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Pred. No. 2.1e-36;
                                                                                                                                                           mRNA
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      Bovidae;
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Best Local Simi
Matches 254;
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                                                                                                                                                                                                                                                                            GTACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGA 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGGCCTCTTGCTGTGGGCTGAGCACCACCTGGCTCAGTTGGCCTTCTGGCC 60
                                                                                                                                                                                                                                                      CACATGGGTCCAAAGGCCTCCCCACCAGGAGGGCATTGGCCTTGGAAGGGA
                                                                                                                                                                                                                                                                                                                                                       ACTGGGCATGTCCGGGGCAGGGAGCTGAAAAGGACTCCACCGCTGCCCTCCTGGAACTGCT 1318
                                                                                                                                                                                                                                                                                                                                                                                                              GTACCCCCAGCTGCTCACCGCCTGGGACGTCTCTTGCTGGAAGAGGGCAGCTTCCACTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTACCCCCAGCTGCTCTACCGCCTGGGGGCGTCTCCTGCTAGAAGAGGGCAGCTTCCACCC 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCGACTGTTTCACAGCTTGGCGTGGGGCACCTGGACCCCAGGGGAGGGTGTGCACTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCCGGGGGAGGGTGTGCATTG 1198
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                                                                           AA628967
AA628967.1
                                                                                                           AA628967 753 bp mRNA EST 16-OCT-1997 af28h06.sl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1033019 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovinae; Bos.

1 (bases 1 to 291)

Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGADACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
BACKWARD: GTTTTCCCAGTCAGGACG
BPlate: 37 row: N column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
On Mar 10, 1998 th
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 14.3%;
Similarity 87.3%;
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mar 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    embryos."
92 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Library made from pooled tissue from day 20 and deembroos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                               GI:2541354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.9e

O; Mismatches
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les 37;
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Best Local Similarity
Matches 214; Conserv
ORGANISM
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                                                                                                                                                                                                                                                                            1582 GTTTTCATACTC-TGCCTCCCCCATTGGGAGGGCCCATTCC 1621
                                                                                                                                                                                                                                                                                                                                                                1522 CTCTCCTAGAGACCTTGAGGCTGGCACGGCGACTCCCAACTCAGCCTGCTCTCACCTACGA 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1462 CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCT 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1402 CCTCTGCCATGAAGATACACCATTGAGACTTGAGACTGGGCAACACCAGCGTCCCCCCACCCG 1461
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                                                                                                                                                                                                                                                        490
                                                                                                                                                                                                                                                                                                                                                                                                                              610 CGTCGTGGTGGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCT 551
                                                                                                                                                                                                                                                        GTTTTCATACTCGTGCCTCCCCATTGGGGAGGGCCCCATTCC
                                                                             AI958076
fc90e01.y1
TR:Q92008 (
AI958076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 753)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Karizman,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
Danio rerio
                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407418
                      zebrafish.
                                                              A1958076.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
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                                                                                                 6 406 bp mRNA EST 20-AUG...yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5'08 Q92008 VHH-1 PRECURSOR ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_hosf-"DH10B"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand polylinker form mRNA obtained from pooled 8-9 week was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (total)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1033019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%;
96.8%;
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Pred. No. 8.4e-30;
0; Mismatches 6
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                                                                                                                            similar to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;

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Best Local Similarity
Matches 224; Conser
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       148
                                                     215
                                                                                                                                                 155 CAGCCGCCGGCGACCGCAAACTCGTGCCGCCTACAAGCAGTTCAGCCCCAA 214
                                                                                                       88
TGTCGAGGAGAAGACCTTATGGGCCAGCGGCAGATACAAGGGCCATGATAACGCGCCAATTA 207
                                                  CGGCAGACTAAGACATCCGAAGATGCTGACACCTCTCGTCTACAAGCGGTTCATACCTAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watererton, B. and Wilson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3188836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.rzpd.de
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                                                                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                              10.6%;
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                                                                                                                                                                                                                           Score 171.2; DB 63; Pred. No. 2.4e-24;
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                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                         88;
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459 GGGCCGGGTCGGGTGGTGGGCA--CCGCCGCGACCGCCAAACTCGTGCCGCTCCGCC 402

GGGCCGGGTCGGGTGGTGGGCAGCCGCCGCCACGCAAACTCGTGCCGCTCGCC 194

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135

Query Match Best Local Matches 17

Similarity

9.7%; 96.1%;

Score 158; D: Pred. No. 9.80; Mismatches

DB 41;).8e-22; nes 5;

Indels

2;

Gaps

Conservative

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AUTHORS
TITLE
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VERSION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 CATCTATGTAATGAACCACTGGCCAGTCGTTAAGCTGCGTGAGACGGCTGAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GGAGAGATTGAAAGAACTTACTCCATATTACAATGCCGACATTATCTTTAAGGATGAGGA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIO15155 459 bp mRNA EST 27-AUG-1998 ot70h05.s1 Soares tottal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622169 3' similar to TR:Q98938 Q98938 INDIAN HEDGEHOG PROTEIN. ; mRNA sequence.

AIO15155
                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 615 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 392.
                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 615 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 12, 1996 this sequence version replaced gi:1405079 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   106
                 Ø
       /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                /clone="IMAGE:1622169"
                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                     'db_xref="taxon:
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TITLE
                                                                                                                                               Query Match
Best Local :
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163 GGCGACCGCCACGCA---AACTCGTGCCGCCTCGCCTACAAGCAGTTCAGCCCCAATGTGC 219
                                            426
                                                           103 TGCTGCTGGTGGTGCCGGGCATGGGGCTGGGGCCGGGTGGGGTGGGCAGCCGGC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version
Other_ESTs: mullg06.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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AI666359
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Eutheria; Rodentia;
1 (bases 1 to 463)
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                                                                                                                                             7.4%;
Similarity 68.0%;
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                  3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

124 c 138 g 113 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_thymus_2NbMT"
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                                                                                                                     Score 119.4; DB 49; Length 463; Pred. No. 3.6e-14; 0; Mismatches 82; Indels 3;
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Mus musculus cDNA clone IMAGE:639130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 CCGAGCGGACCCTGGGCCGAGTGGGCCAGCGGGGGGGGGTAACAAGGGGGTCGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCAAGGAGCTCACCCCCAATTACAATCCAGCACATCATCTTCAAGGACGAGGAGAACA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 537)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
(1997)
(Inpublished (1997)
(On May 18, 1998 this sequence version replaced gi:3137802.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
AI645932
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                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 478
                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI645932.1 GI:4724407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ouse mouse.
              107
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                            /tissue_type="Thymus"
/dev_stage="4 weeks"
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Query Match Best Local Similarity

7.1%; 67.3%;

Score 115.6; DB 49; Pred. No. 2.1e-13;

Length 537;

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RESULT 1
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1 (bases 1 to 314)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Chissoe,S., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Hawkins,M., Hultman,M., Kucaba,T., Parange,C., Rifkin,L.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlflug,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                               On May 9, 1995 this sequence version rep. Contact: Wilson RK
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zml3f08.sl Stratagene pancreas (#937208) Homo sapiens cDNA cla
IMAGE:525543 3' similar to TR:G443942 G443942 DESERT HEDGEHOG
PRECURSOR. ;, mRNA sequence.
                                                                                                                                                  rossible reversed clone: polyT not found Insert Length: 862 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found Possible reversed clone: polyT not found Insert Length: 862 Std Error: 0.000
                                                                                                                                                                                                                                                                                               WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Marra, M.
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314 286 1810
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                                                                                                                                          quality sequence stop: 283.
                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1995 this sequence version replaced gi:802645
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                                                                                                                          Pocat
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BACR19D16 of RPCI-98 library from
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                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:4934461
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/lab_host="SOLR cells (kanamycin resistant)"
                                 Site_1:
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Score 81.8; DB 20,
Pred. No. 7.8e-07;
  Indels
              Length
  0,
 Gaps
  0
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1050 AAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGAC 1109 930 TTTGCCAGCCACGTGCAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGCAG 989 CACCACCIGGCICAGITGGCCCITCTGGCCCCTGAGACTCITTCAC 1154 GCGCACGGGACGCTGCTGGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGT CCAGCGCGCGTGGCCCGTGTGGCGCGGGAGGAAGCCGTGGNGTNGTTCGCGCCGCTCACC CCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACA 1049 TTCGCGCGCCGGCTACGCCTNGGGGGACTCGGTGCTGGCGCCCCGGCGGGGATGCGCTTCGG 95

survey sequence TET3 end of BAC # rom Drosophila melanogaster (fruit 03-JUN-1999

260 •

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[bases 1 to 925)

AL Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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                                                                                                                                                                                                                                                      Email: egreen@nhgri.nih.gov
Plate: 05 row: E column: 11
Seq primer: -21M13 (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 27
Tel: 3014020201
Fax: 301402473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D. 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 288)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jan 25, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 7 (3), 281-292 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Eric D. Green
/Glone_lib="Chromosome 7 Fetal Brain cDNA Library"
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/tissue_type="brain"
/dev_stage="pool of 9 week and 12 week"
/lab_host="E. coli strain DH5 alpha"
/note="Organ: brain; Vector: paMPLO; CDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="end : TET3"
61 c 61 g
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7B05E11"
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13.0%; Pred. No. 0.0045;
ative 155; Mismatches 105;
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Some 7 Fetal Brain cDNA Library Homo sapiens cDNA
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Matches 104; Conservative
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